



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 126843

TO: Patricia Duffy
Location: rem/3b05/3c18
Art Unit: 1645
Monday, July 19, 2004

Case Serial Number: 09/932613

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Duffy,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

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STIC-Biotech/ChemLib

126843

my

From: Duffy, Patricia
Sent: Sunday, July 11, 2004 10:30 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search 09/932,613

Importance: High

Please search SEQ ID NO:457 in the commercial and interference databases.
Please print out top 100 hits.

Thanks.

Patricia A. Duffy, Ph.D.
Art Unit 1645, Remsen 3B05
571-272-0855

STIC
JUL 12 2004
10:30 AM

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 21:21:26 ; Search time 54 Seconds

(without alignments)
52.324 Million cell updates/sec

Title: US-09-932-613-457

Perfect score: 64

Sequence: 1 WYDPLTKML 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*\n2: geneseqp2000s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	10	5	ABJ00997 B lymphoc
2	64	100.0	10	5	ABJ00977 B lymphoc
3	64	100.0	10	5	ABG33859 B lymphoc
4	64	100.0	10	5	ABG33858 B lymphoc
5	64	100.0	12	5	ABJ00996 B lymphoc
6	64	100.0	12	5	ABG33858 B lymphoc
7	64	100.0	13	5	ABJ00980 B lymphoc
8	64	100.0	13	5	ABG33841 B lymphoc
9	64	100.0	14	5	ABJ00739 B lymphoc
10	64	100.0	14	5	ABJ00744 B lymphoc
11	64	100.0	14	5	ABJ00770 B lymphoc
12	64	100.0	14	5	ABJ00791 B lymphoc
13	64	100.0	14	5	ABJ00793 B lymphoc
14	64	100.0	14	5	ABJ00818 B lymphoc
15	64	100.0	14	5	ABJ00826 B lymphoc
16	64	100.0	14	5	ABJ00836 B lymphoc
17	64	100.0	14	5	ABJ00794 B lymphoc
18	64	100.0	14	5	ABJ00821 B lymphoc
19	64	100.0	14	5	ABJ00832 B lymphoc
20	64	100.0	14	5	ABJ00731 B lymphoc
21	64	100.0	14	5	ABJ00773 B lymphoc
22	64	100.0	14	5	ABJ00809 B lymphoc
23	64	100.0	14	5	ABJ00816 B lymphoc
24	64	100.0	14	5	ABJ00822 B lymphoc
25	64	100.0	14	5	ABJ00830 B lymphoc

26	64	100.0	14	5	ABJ00831 B lymphoc
27	64	100.0	14	5	ABJ00730 B lymphoc
28	64	100.0	14	5	ABJ00738 B lymphoc
29	64	100.0	14	5	ABJ00754 B lymphoc
30	64	100.0	14	5	ABJ00777 B lymphoc
31	64	100.0	14	5	ABJ00835 B lymphoc
32	64	100.0	14	5	ABJ00771 B lymphoc
33	64	100.0	14	5	ABJ00798 B lymphoc
34	64	100.0	14	5	ABJ00803 B lymphoc
35	64	100.0	14	5	ABJ00827 B lymphoc
36	64	100.0	14	5	ABJ00833 B lymphoc
37	64	100.0	14	5	ABJ00737 B lymphoc
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39	64	100.0	14	5	ABJ00760 B lymphoc
40	64	100.0	14	5	ABJ00786 B lymphoc
41	64	100.0	14	5	ABJ00802 B lymphoc
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44	64	100.0	14	5	ABJ00729 B lymphoc
45	64	100.0	14	5	ABJ00756 B lymphoc
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47	64	100.0	14	5	ABJ00790 B lymphoc
48	64	100.0	14	5	ABJ00792 B lymphoc
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63	64	100.0	14	5	ABJ00735 B lymphoc
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65	64	100.0	14	5	ABJ00749 B lymphoc
66	64	100.0	14	5	ABJ00762 B lymphoc
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68	64	100.0	14	5	ABJ00775 B lymphoc
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89	64	100.0	14	5	ABJ00767 B lymphoc
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91	64	100.0	14	5	ABJ00795 B lymphoc
92	64	100.0	14	5	ABJ00804 B lymphoc
93	64	100.0	14	5	ABJ00820 B lymphoc
94	64	100.0	14	5	ABJ00828 B lymphoc
95	64	100.0	14	5	ABJ00734 B lymphoc
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97	64	100.0	14	5	ABJ00745 B lymphoc
98	64	100.0	14	5	ABJ00759 B lymphoc

99	64	100.0	14	5	ABJ00778	ABJ00778 B	Lymphoc	172	64	100.0	14	5	ABG33576	ABg33576 B	Lymphoc
100	64	100.0	14	5	ABJ00796	ABJ00796 B	Lymphoc	173	64	100.0	14	5	ABG33591	ABg33591 B	Lymphoc
101	64	100.0	14	5	ABJ00810	ABJ00810 B	Lymphoc	174	64	100.0	14	5	ABG33594	ABg33594 B	Lymphoc
102	64	100.0	14	5	ABJ00837	ABJ00837 B	Lymphoc	175	64	100.0	14	5	ABG33623	ABg33623 B	Lymphoc
103	64	100.0	14	5	ABJ00746	ABJ00746 B	Lymphoc	176	64	100.0	14	5	ABG33629	ABg33629 B	Lymphoc
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105	64	100.0	14	5	ABJ00764	ABJ00764 B	Lymphoc	178	64	100.0	14	5	ABG33635	ABg33635 B	Lymphoc
106	64	100.0	14	5	ABJ00783	ABJ00783 B	Lymphoc	179	64	100.0	14	5	ABG33688	ABg33688 B	Lymphoc
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108	64	100.0	14	5	ABJ00801	ABJ00801 B	Lymphoc	181	64	100.0	14	5	ABG33621	ABg33621 B	Lymphoc
109	64	100.0	14	5	ABJ00823	ABJ00823 B	Lymphoc	182	64	100.0	14	5	ABG33628	ABg33628 B	Lymphoc
110	64	100.0	14	5	ABJ00727	ABJ00727 B	Lymphoc	183	64	100.0	14	5	ABG33671	ABg33671 B	Lymphoc
111	64	100.0	14	5	ABJ00733	ABJ00733 B	Lymphoc	184	64	100.0	14	5	ABG33674	ABg33674 B	Lymphoc
112	64	100.0	14	5	ABJ00748	ABJ00748 B	Lymphoc	185	64	100.0	14	5	ABG33589	ABg33589 B	Lymphoc
113	64	100.0	14	5	ABJ00753	ABJ00753 B	Lymphoc	186	64	100.0	14	5	ABG33600	ABg33600 B	Lymphoc
114	64	100.0	14	5	ABJ00765	ABJ00765 B	Lymphoc	187	64	100.0	14	5	ABG33611	ABg33611 B	Lymphoc
115	64	100.0	14	5	ABJ00768	ABJ00768 B	Lymphoc	188	64	100.0	14	5	ABG33654	ABg33654 B	Lymphoc
116	64	100.0	14	5	ABJ00797	ABJ00797 B	Lymphoc	189	64	100.0	14	5	ABG33659	ABg33659 B	Lymphoc
117	64	100.0	14	5	ABJ00800	ABJ00800 B	Lymphoc	190	64	100.0	14	5	ABG33654	ABg33654 B	Lymphoc
118	64	100.0	14	5	ABJ00805	ABJ00805 B	Lymphoc	191	64	100.0	14	5	ABG33655	ABg33655 B	Lymphoc
119	64	100.0	14	5	ABJ00808	ABJ00808 B	Lymphoc	192	64	100.0	14	5	ABG33596	ABg33596 B	Lymphoc
120	64	100.0	14	5	ABJ00813	ABJ00813 B	Lymphoc	193	64	100.0	14	5	ABG33615	ABg33615 B	Lymphoc
121	64	100.0	14	5	ABJ00814	ABJ00814 B	Lymphoc	194	64	100.0	14	5	ABG33824	ABg33824 B	Lymphoc
122	64	100.0	14	5	ABG33595	ABg33595 B	Lymphoc	195	64	100.0	14	5	ABG33652	ABg33652 B	Lymphoc
123	64	100.0	14	5	ABG33606	ABg33606 B	Lymphoc	196	64	100.0	14	5	ABG33666	ABg33666 B	Lymphoc
124	64	100.0	14	5	ABG33616	ABg33616 B	Lymphoc	197	64	100.0	14	5	ABG33678	ABg33678 B	Lymphoc
125	64	100.0	14	5	ABG33642	ABg33642 B	Lymphoc	198	64	100.0	14	5	ABG33684	ABg33684 B	Lymphoc
126	64	100.0	14	5	ABG33656	ABg33656 B	Lymphoc	199	64	100.0	14	5	ABG33689	ABg33689 B	Lymphoc
127	64	100.0	14	5	ABG33663	ABg33663 B	Lymphoc	200	64	100.0	14	5	ABG33696	ABg33696 B	Lymphoc
128	64	100.0	14	5	ABG33667	ABg33667 B	Lymphoc	201	64	100.0	14	5	ABG33588	ABg33588 B	Lymphoc
129	64	100.0	14	5	ABG33598	ABg33598 B	Lymphoc	202	64	100.0	14	5	ABG33603	ABg33603 B	Lymphoc
130	64	100.0	14	5	ABG33640	ABg33640 B	Lymphoc	203	64	100.0	14	5	ABG33618	ABg33618 B	Lymphoc
131	64	100.0	14	5	ABG33644	ABg33644 B	Lymphoc	204	64	100.0	14	5	ABG33659	ABg33659 B	Lymphoc
132	64	100.0	14	5	ABG33679	ABg33679 B	Lymphoc	205	64	100.0	14	5	ABG33648	ABg33648 B	Lymphoc
133	64	100.0	14	5	ABG33697	ABg33697 B	Lymphoc	206	64	100.0	14	5	ABG33609	ABg33609 B	Lymphoc
134	64	100.0	14	5	ABG33632	ABg33632 B	Lymphoc	207	64	100.0	14	5	ABG33685	ABg33685 B	Lymphoc
135	64	100.0	14	5	ABG33632	ABg33632 B	Lymphoc	208	64	100.0	14	5	ABG33694	ABg33694 B	Lymphoc
136	64	100.0	14	5	ABG33639	ABg33639 B	Lymphoc	209	64	100.0	14	5	ABG33592	ABg33592 B	Lymphoc
137	64	100.0	14	5	ABG33643	ABg33643 B	Lymphoc	210	64	100.0	14	5	ABG33614	ABg33614 B	Lymphoc
138	64	100.0	14	5	ABG33665	ABg33665 B	Lymphoc	211	64	100.0	14	5	ABG33667	ABg33667 B	Lymphoc
139	64	100.0	14	5	ABG33677	ABg33677 B	Lymphoc	212	64	100.0	14	5	ABG33637	ABg33637 B	Lymphoc
140	64	100.0	14	5	ABG33681	ABg33681 B	Lymphoc	213	64	100.0	14	5	ABG33664	ABg33664 B	Lymphoc
141	64	100.0	14	5	ABG33698	ABg33698 B	Lymphoc	214	64	100.0	14	5	ABG33675	ABg33675 B	Lymphoc
142	64	100.0	14	5	ABG33602	ABg33602 B	Lymphoc	215	64	100.0	14	5	ABG33687	ABg33687 B	Lymphoc
143	64	100.0	14	5	ABG33619	ABg33619 B	Lymphoc	216	64	100.0	14	5	ABG33593	ABg33593 B	Lymphoc
144	64	100.0	14	5	ABG33636	ABg33636 B	Lymphoc	217	64	100.0	14	5	ABG33599	ABg33599 B	Lymphoc
145	64	100.0	14	5	ABG33641	ABg33641 B	Lymphoc	218	64	100.0	14	5	ABG33601	ABg33601 B	Lymphoc
146	64	100.0	14	5	ABG33661	ABg33661 B	Lymphoc	219	64	100.0	14	5	ABG33612	ABg33612 B	Lymphoc
147	64	100.0	14	5	ABG33670	ABg33670 B	Lymphoc	220	64	100.0	14	5	ABG33625	ABg33625 B	Lymphoc
148	64	100.0	14	5	ABG33683	ABg33683 B	Lymphoc	221	64	100.0	14	5	ABG33613	ABg33613 B	Lymphoc
149	64	100.0	14	5	ABG33683	ABg33683 B	Lymphoc	222	64	100.0	14	5	ABG33629	ABg33629 B	Lymphoc
150	64	100.0	14	5	ABG33670	ABg33670 B	Lymphoc	223	64	100.0	14	5	ABG33669	ABg33669 B	Lymphoc
151	64	100.0	14	5	ABG33683	ABg33683 B	Lymphoc	224	64	100.0	14	5	ABG33680	ABg33680 B	Lymphoc
152	64	100.0	14	5	ABG33607	ABg33607 B	Lymphoc	225	64	100.0	14	5	ABG33686	ABg33686 B	Lymphoc
153	64	100.0	14	5	ABG33672	ABg33672 B	Lymphoc	226	64	100.0	14	5	ABG33624	ABg33624 B	Lymphoc
154	64	100.0	14	5	ABG33673	ABg33673 B	Lymphoc	227	64	100.0	14	5	ABG33604	ABg33604 B	Lymphoc
155	64	100.0	14	5	ABG33682	ABg33682 B	Lymphoc	228	64	100.0	14	5	ABG33646	ABg33646 B	Lymphoc
156	64	100.0	14	5	ABG33692	ABg33692 B	Lymphoc	229	64	100.0	14	5	ABG33647	ABg33647 B	Lymphoc
157	64	100.0	14	5	ABG33699	ABg33699 B	Lymphoc	230	64	100.0	14	5	ABG33668	ABg33668 B	Lymphoc
158	64	100.0	14	5	ABG33605	ABg33605 B	Lymphoc	231	64	100.0	14	5	ABG33690	ABg33690 B	Lymphoc
159	64	100.0	14	5	ABG33608	ABg33608 B	Lymphoc	232	64	100.0	14	5	ABJ00979	ABJ00979 B	Lymphoc
160	64	100.0	14	5	ABG33617	ABg33617 B	Lymphoc	233	64	100.0	14	5	ABG33840	ABg33840 B	Lymphoc
161	64	100.0	14	5	ABG33626	ABg33626 B	Lymphoc	234	64	100.0	14	5	ABJ00978	ABJ00978 B	Lymphoc
162	64	100.0	14	5	ABG33633	ABg33633 B	Lymphoc	235	64	100.0	14	5	ABJ00981	ABJ00981 B	Lymphoc
163	64	100.0	14	5	ABG33650	ABg33650 B	Lymphoc	236	64	100.0	14	5	ABJ00982	ABJ00982 B	Lymphoc
164	64	100.0	14	5	ABG33651	ABg33651 B	Lymphoc	237	64	100.0	14	5	ABG33842	ABg33842 B	Lymphoc
165	64	100.0	14	5	ABG33657	ABg33657 B	Lymphoc	238	64	100.0	14	5	ABJ00926	ABJ00926 B	Lymphoc
166	64	100.0	14	5	ABG33658	ABg33658 B	Lymphoc	239	62	96.9	14	5	ABJ00927	ABJ00927 B	Lymphoc
167	64	100.0	14	5	ABG33662	ABg33662 B	Lymphoc	240	62	96.9	14	5			
168	64	100.0	14	5	ABG33693	ABg33693 B	Lymphoc	241	62	96.9	14	5			
169	64	100.0	14	5	ABG33695	ABg33695 B	Lymphoc	242	62	96.9	14	5			
170	64	100.0	14	5	ABG33653	ABg33653 B	Lymphoc	243	62	96.9	14	5			
171	64	100.0	14	5	ABG33653	ABg33653 B	Lymphoc	244	62	96.9	14	5			

XX OS Unidentified.
 XX XX
 PN WO200216411-A2.
 XX XX
 PD 28-FEB-2002.
 XX XX
 PF 17-AUG-2001; 2001WO-US025850.
 XX XX
 PR 18-AUG-2000; 2000US-0226700P.
 XX XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX XX
 PI Belzter JP, Potter DM, Fleming TL, Rosen CA;
 XX XX
 DR WPI; 2002-499775/53.
 XX XX
 PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide.
 XX XX
 PS Example 11; Page 377; 387pp; English.
 XX XX
 CC The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving immunoglobulin production, B cell proliferation
 CC The Blys binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 XX XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 64; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 |||||
 DB 1 WYDPLTKLWL 10

RESULT 3
 ABG33859
 ID ABG33859 standard; peptide; 10 AA.
 XX XX
 AC ABG33859;
 XX XX
 DT 15-JUL-2002 (first entry)
 XX XX
 DE B Lymphocyte Stimulator (Blys) binding peptide #433.
 XX XX
 KW B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide;
 KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
 KW synovial fluid; saliva; mucus.
 XX XX
 OS Synthetic.
 XX XX
 PN WO200216412-A2.
 XX XX
 PD 28-FEB-2002.
 XX XX
 PF 17-AUG-2001; 2001WO-US025891.
 XX XX
 PR 18-AUG-2000; 2000US-0226489P.
 XX XX
 PA (DYAX-) DYAX CORP.
 XX XX

PI Belzter JP, Potter MD, Fleming TJ, Ladner RC;
 XX XX
 DR WPI; 2002-351647/38.
 XX XX
 PT New B-lymphocyte stimulator binding polypeptide useful in detecting or
 PT isolating Blys or Blys-like polypeptide comprises a specified amino acid
 PT sequence.
 XX XX
 PS Claim 8; Page 98; 269pp; English.
 XX XX
 CC The invention relates to a B lymphocyte stimulator (Blys) binding
 CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins
 CC reversibly or irreversibly. The binding peptides are used in detection,
 CC isolation and/or purification of Blys in a solution such as water or a
 CC buffer solution, as well as any fluid and/or cell obtained from an
 CC individual biological fluid, body tissue, body cell, cell line, tissue
 CC culture or other source containing Blys or Blys-like polypeptides. The
 CC biological fluids include: sera, plasma, lymph, blood, blood fraction,
 CC urine, synovial fluid, spinal fluid, saliva and mucus. Sequences
 CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
 CC ABG33852-33862 represent Blys binding peptides of the invention
 XX XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 64; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 |||||
 DB 1 WYDPLTKLWL 10

RESULT 4
 ABG33838
 ID ABG33838 standard; peptide; 10 AA.
 XX XX
 AC ABG33838;
 XX XX
 DT 15-JUL-2002 (first entry)
 XX XX
 DE B Lymphocyte Stimulator (Blys) binding peptide #414.
 XX XX
 KW B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide;
 KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
 KW synovial fluid; saliva; mucus.
 XX XX
 OS Synthetic.
 XX XX
 PN WO200216412-A2.
 XX XX
 PD 28-FEB-2002.
 XX XX
 PF 17-AUG-2001; 2001WO-US025891.
 XX XX
 PR 18-AUG-2000; 2000US-0226489P.
 XX XX
 PA (DYAX-) DYAX CORP.
 XX XX
 PI Belzter JP, Potter MD, Fleming TJ, Ladner RC;
 XX XX
 DR WPI; 2002-351647/38.
 XX XX
 PT New B-lymphocyte stimulator binding polypeptide useful in detecting or
 PT isolating Blys or Blys-like polypeptide comprises a specified amino acid
 PT sequence.
 XX XX
 PS Claim 4; Page 97; 269pp; English.
 XX XX
 CC The invention relates to a B lymphocyte stimulator (Blys) binding
 CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins
 CC reversibly or irreversibly. The binding peptides are used in detection,
 CC isolation and/or purification of Blys in a solution such as water or a

CC buffer solution, as well as any fluid and/or cell obtained from an
CC individual biological fluid, body tissue, body cell, cell line, tissue
CC culture or other source containing Blys or Blys-like polypeptides. The
CC biological fluid include sera, plasma, lymph, blood, blood fraction,
CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
CC ABG33852-33862 represent Blys binding peptides of the invention
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 64; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLWL 10
DB 1 WYDPLTKLWL 10
RESULT 5
ABJ00996
ID ABJ00996 standard; peptide; 12 AA.
XX
AC ABJ00996;
XX
DT 05-SEP-2002 (first entry)
XX
DE B lymphocyte stimulator protein binding peptide #167.
XX
KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cystostatic; immunostimulant; antitumour; anti-HIV;
KW antiasthmatic; antiallergic; thymimetic; antianaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
PN WO200216411-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
DR WPI; 2002-499775/53.
XX
PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
PS Claim 71; Page 236; 387pp; English.
XX
CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide

XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 64; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLWL 10
DB 1 WYDPLTKLWL 10
RESULT 6
ABG33858
ID ABG33858 standard; peptide; 12 AA.
XX
AC ABG33858;
XX
DT 15-JUL-2002 (first entry)
XX
DE B lymphocyte stimulator (Blys) binding peptide #432.
XX
KW B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;
KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
KW synovial fluid; saliva; mucus.
XX
OS Synthetic.
XX
PN WO200216412-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025891.
XX
PR 18-AUG-2000; 2000US-0226489P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
XX
DR WPI; 2002-351647/38.
XX
PT New B-lymphocyte stimulator binding polypeptide useful in detecting or
PT isolating Blys or Blys-like polypeptide comprises a specified amino acid
PT sequence.
PS Claim 8; Page 98; 269pp; English.
XX
CC The invention relates to a B lymphocyte stimulator (Blys) binding
CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins
CC reversibly or irreversibly. The binding peptides are used in detection,
CC isolation and/or purification of Blys in a solution such as water or a
CC buffer solution, as well as any fluid and/or cell obtained from an
CC individual biological fluid, body tissue, body cell, cell line, tissue
CC culture or other source containing Blys or Blys-like polypeptides. The
CC biological fluids include sera, plasma, lymph, blood, blood fraction,
CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
CC ABG33852-33862 represent Blys binding peptides of the invention
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 64; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLWL 10
DB 1 WYDPLTKLWL 10
RESULT 7
ABJ00980

ID ABJ00980 standard; peptide; 13 AA.
 XX
 AC ABJ00980;
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE B lymphocyte affinity maturation library peptide#253.
 XX
 KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;
 KW antiaesthetic; antiallergic; thyromimetic; antinaemic; haemostatic;
 KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX
 OS Unidentified.
 XX
 PN WO200216411-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-US025850.
 XX
 PR 18-AUG-2000; 2000US-0226700P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Beltzer JP, Potter DM, Fleming TJ, Rosen CA;
 XX
 DR WPI; 2002-499775/53.
 XX
 PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide.
 XX
 PS Example 11; Page 220; 387pp; English.
 XX
 CC The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of Blys binding polypeptide.
 CC The Blys binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 64; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00087;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WYDPLTKLWL 10
 DB 1 WYDPLTKLWL 10
 RESULT 8
 ABG33841
 ID ABG33841 standard; peptide; 13 AA.
 XX
 AC ABG33841;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE B lymphocyte stimulator (Blys) binding peptide #417.

XX
 KW B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;
 KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
 KW synovial fluid; saliva; mucus.
 XX
 OS Synthetic.
 XX
 PN WO200216412-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-US025891.
 XX
 PR 18-AUG-2000; 2000US-0226489P.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
 XX
 DR WPI; 2002-351647/38.
 XX
 PT New B-lymphocyte stimulator binding polypeptide useful in detecting or
 PT isolating Blys or Blys-like polypeptide comprises a specified amino acid
 PT sequence.
 XX
 PS Claim 7; Page 94; 269pp; English.
 XX
 CC The invention relates to a B lymphocyte stimulator (Blys) binding
 CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins
 CC reversibly or irreversibly. The binding peptides are used in detection,
 CC isolation and/or purification of Blys in a solution such as water or a
 CC buffer solution, as well as any fluid and/or cell obtained from an
 CC individual biological fluid, body tissue, body cell, cell line, tissue
 CC culture or other source containing Blys or Blys-like polypeptides. The
 CC biological fluids include sera, plasma, lymph, blood, blood fraction,
 CC urine, synovial fluid, spinal fluid, saliva and mucus. Sequences
 CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
 CC ABG33852-33862 represent Blys binding peptides of the invention
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 64; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00087;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WYDPLTKLWL 10
 DB 1 WYDPLTKLWL 10
 RESULT 9
 ABJ00739
 ID ABJ00739 standard; peptide; 14 AA.
 XX
 AC ABJ00739;
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE B lymphocyte affinity maturation library peptide #13.
 XX
 KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;
 KW antiaesthetic; antiallergic; thyromimetic; antinaemic; haemostatic;
 KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX
 OS Unidentified.
 XX
 PN WO200216411-A2.

XX 28-FEB-2002.
XX 17-AUG-2001; 2001WO-US025850.
XX 18-AUG-2000; 2000US-0226700P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;
XX WPI; 2002-499775/53.
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.
XX Claim 70; Page 214; 387pp; English.
XX The present invention relates to the treatment, prevention or
XX amelioration of a disease or disorder associated with: aberrant B
XX lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
XX of haematopoietic origin; or proliferative disease; and reducing,
XX inhibiting or stimulating immunoglobulin production, B cell proliferation
XX and graft rejection involving administration of Blys binding polypeptide.
XX The Blys binding polypeptides are used in the treatment, prevention or
XX amelioration of diseases such as immune system diseases, proliferative
XX diseases, diseases of cells of hematopoietic origin, graft rejection,
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX neurodegenerative diseases. The present sequence is a B lymphocyte
XX stimulator protein binding peptide
XX Sequence 14 AA:
SQ
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12
RESULT 10
ABJ00744 ID ABJ00744 standard; peptide; 14 AA.
XX AC ABJ00744;
XX DT 05-SEP-2002 (first entry)
XX DE B lymphocyte affinity maturation library peptide #18.
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
XX allergy; proliferative disease; infectious disease; arteriosclerosis;
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX ischaemia; graft-versus-host disease; neurodegenerative disease;
XX immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
XX neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
XX antiaesthetic; anti-allergic; thymimetic; antianemic; haemostatic;
XX dermatological; anti-inflammatory; cardiant; ophthalmological; uropathic;
XX antidiabetic; antithyroid; antidepressant; hepatotropic.
XX OS Unidentified.
XX WO200216411-A2.
XX 28-FEB-2002.
XX 17-AUG-2001; 2001WO-US025850.
XX PF 18-AUG-2000; 2000US-0226700P.
XX PR 18-AUG-2000; 2000US-0226700P.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;
XX WPI; 2002-499775/53.
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.
XX Claim 70; Page 214; 387pp; English.
XX The present invention relates to the treatment, prevention or
XX amelioration of a disease or disorder associated with: aberrant B
XX lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
XX of haematopoietic origin; or proliferative disease; and reducing,
XX inhibiting or stimulating immunoglobulin production, B cell proliferation
XX and graft rejection involving administration of Blys binding polypeptide.
XX The Blys binding polypeptides are used in the treatment, prevention or
XX amelioration of diseases such as immune system diseases, proliferative
XX diseases, diseases of cells of hematopoietic origin, graft rejection,
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX neurodegenerative diseases. The present sequence is a B lymphocyte
XX stimulator protein binding peptide
XX Sequence 14 AA:
SQ
Query Match. 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12
RESULT 11
ABJ00770 ID ABJ00770 standard; peptide; 14 AA.
XX AC ABJ00770;
XX DT 05-SEP-2002 (first entry)
XX DE B lymphocyte affinity maturation library peptide #44.
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
XX allergy; proliferative disease; infectious disease; arteriosclerosis;
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX ischaemia; graft-versus-host disease; neurodegenerative disease;
XX immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
XX neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
XX antiaesthetic; anti-allergic; thymimetic; antianemic; haemostatic;
XX dermatological; anti-inflammatory; cardiant; ophthalmological; uropathic;
XX antidiabetic; antithyroid; antidepressant; hepatotropic.
XX OS Unidentified.
XX WO200216411-A2.
XX 28-FEB-2002.
XX 17-AUG-2001; 2001WO-US025850.
XX PF 18-AUG-2000; 2000US-0226700P.
XX PR (HUMA-) HUMAN GENOME SCI INC.
XX PA Belzter JP, Potter DM, Fleming TL, Rosen CA;
XX WPI; 2002-499775/53.
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises

PT	administering B lymphocyte stimulator binding polypeptide.
XX	
PS	Claim 70; Page 215; 387pp; English.
XX	
CC	The present invention relates to the treatment, prevention or
CC	amelioration of a disease or disorder associated with: aberrant B
CC	lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells
CC	of haematopoietic origin; or proliferative disease; and reducing,
CC	inhibiting or stimulating immunoglobulin production, B cell proliferation
CC	and graft rejection involving administration of BLyS binding polypeptide.
CC	The BLyS binding polypeptides are used in the treatment, prevention or
CC	amelioration of diseases such as immune system diseases, proliferative
CC	diseases, infectious diseases of cells of haematopoietic origin, graft rejection,
CC	allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC	hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC	neurodegenerative diseases. The present sequence is a B lymphocyte
CC	stimulator protein binding peptide
CC	
SQ	Sequence 14 AA;
QY	1 WYDPLTKML 10
Db	3 WYDPLTKML 12
RESULT 12	
ID	ABJ00791
AC	ABJ00791 standard; peptide; 14 AA.
XX	
AC	ABJ00791;
XX	
DT	05-SEP-2002 (first entry)
DE	
XX	
XX	
B	lymphocyte affinity maturation library peptide #65.
B	lymphocyte stimulator protein binding protein; BLyS; immune disease;
allergy; proliferative disease; infectious disease; arteriosclerosis;	
inflammatory disorder; hypergammaglobulinaemia; blood clotting;	
ischaemia; graft-versus-host disease; neurodegenerative disease;	
immunosuppressive; nephrotropic; antirheumatic; antiarthritic;	
neuroproliferative; cytostatic; immunostimulant; anti-tumour; anti-HIV;	
antiaesthetic; antiallergic; thyromimetic; antinaemic; haemostatic;	
dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;	
antidiabetic; antithyroid; antidepressant; hepatotropic.	
XX	
OS	Unidentified.
XX	
XX	
PN	WO200216411-A2.
XX	
PD	28-FEB-2002.
XX	
PF	17-AUG-2001; 2001WO-US025850.
XX	
PR	18-AUG-2000; 2000US-0226700P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX	
DR	WPI; 2002-499775/53.
XX	
PT	The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX	administering B lymphocyte stimulator binding polypeptide.
PS	Claim 70; Page 215; 387pp; English.
CC	The present invention relates to the treatment, prevention or
CC	amelioration of a disease or disorder associated with: aberrant B
CC	lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells

CC		of haematopoietic origin; or proliferative disease; and reducing,
CC		inhibiting or stimulating immunoglobulin production; B cell proliferation
CC		and graft rejection involving administration of Blys binding polypeptide.
CC		The Blys binding polypeptides are used in the treatment, prevention or
CC		amelioration of diseases such as immune system diseases, proliferative
CC		diseases, diseases of cells of haematopoietic origin, graft rejection,
CC		allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC		hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC		neurodegenerative diseases. The present sequence is a B lymphocyte
CC		stimulator protein binding peptide
SQ		Sequence 14 AA;
Df		
Qy	1 WYDPLTKLML 10	
	3 WYDPLTKLML 12	
RESULT 13		
ID	ABJ00793 standard; peptide; 14 AA.	
XX	ABJ00793	
AC	ABJ00793;	
XX		
DT	05-SEP-2002 (first entry)	
DE	B lymphocyte affinity maturation library peptide #67.	
XX		
KW	B lymphocyte stimulator protein binding protein; Blys; immune disease;	
KW	allergy; proliferative diseases; infectious diseases; arteriosclerosis;	
KW	inflammatory disorder; hypergammaglobulinaemia; blood clotting;	
KM	ischaemia; graft-versus-host disease; neurodegenerative disease;	
KW	immunosuppressive; nephrotropic; antirheumatic; antiarthritic;	
KW	neuroprotective; cytostatic; immunostimulant; anticancer; anti-HIV;	
KW	antiaesthetic; anti-allergic; thymometric; antianaemic; haemostatic;	
KW	dermatological; anti-inflammatory; cardiac; ophthalmological; uropathic;	
XX	antidiabetic; antichryoid; antidepressant; hepatotropic.	
OS	Unidentified.	
XX		
PN	WO200216411-A2.	
PD		
PF	17-AUG-2001; 2001WO-US025850.	
PR	18-AUG-2000; 2000US-0226700P.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
I1	Beltzer JP, Potter DM, Fleming TL, Rosen CA;	
DR	WPI; 2002-499775/53.	
PT		
Pt	The treatment of various diseases e.g. rheumatoid arthritis, comprises	
XX	administering B lymphocyte stimulator binding polypeptide.	
PS	Claim 70; Page 215; 387pp; English.	
XX		
CC	The present invention relates to the treatment, prevention or	
CC	amelioration of a disease or disorder associated with: aberrant B	
CC	lymphocyte stimulator (Blys), Blys receptor expression or activity; cells	
CC	of haematopoietic origin; or proliferative disease; and reducing,	
CC	inhibiting or stimulating immunoglobulin production; B cell proliferation	
CC	and graft rejection involving administration of Blys binding polypeptide.	
CC	The Blys binding polypeptides are used in the treatment, prevention or	
CC	amelioration of diseases such as immune system diseases, proliferative	
CC	diseases, diseases of cells of hematopoietic origin, graft rejection,	
CC	allergies, infectious diseases, arteriosclerosis, inflammatory disorders,	

CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10
|||
DB 3 WYDPLTKLML 12

RESULT 14
ABJ00818
ID ABJ00818 standard; peptide; 14 AA.

AC ABJ00818;
XX
DT 05-SEP-2002. (first entry)

DE B lymphocyte affinity maturation library peptide #92.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytotoxic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX Unidentified.

OS WO200216411-A2.

PN 28-FEB-2002.

PD 17-AUG-2001; 2001WO-US025850.

PF 18-AUG-2000; 2000US-0226700P.

PR (HUMA-) HUMAN GENOME SCT INC.

PA Beltzer JP, Potter DM, Fleming TL, Rosen CA;

PI WPI, 2002-499775/53.

DR The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.

PT Claim 70; Page 215; 387pp; English.

XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10
|||
DB 3 WYDPLTKLML 12

RESULT 15
ABJ00826
ID ABJ00826 standard; peptide; 14 AA.

AC ABJ00826;

DT 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #100.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytotoxic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX Unidentified.

OS WO200216411-A2.

PN 28-FEB-2002.

PD 17-AUG-2001; 2001WO-US025850.

PF 18-AUG-2000; 2000US-0226700P.

PR (HUMA-) HUMAN GENOME SCT INC.

PA Beltzer JP, Potter DM, Fleming TL, Rosen CA;

PI WPI, 2002-499775/53.

DR The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.

PT Claim 70; Page 216; 387pp; English.

XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10
|||
DB 3 WYDPLTKLML 12

RESULT 16
 ABJ00836
 ID ABJ00836 standard; peptide; 14 AA.
 XX
 AC ABJ00836;
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE B lymphocyte affinity maturation library peptide #110.
 XX
 KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW neuropsychiatric; cytostatic; immunostimulant; antitumour; anti-HIV;
 KW antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX
 OS Unidentified.
 XX
 PN WO200216411-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-US025850.
 XX
 PR 18-AUG-2000; 2000US-0226700P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
 XX
 DR WPI; 2002-499775/53.
 XX
 PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide.
 XX
 PS Claim 70; Page 216; 387pp; English.
 XX
 CC The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of BlyS binding polypeptide.
 CC The BlyS binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 XX
 SQ Sequence 14 AA;
 XX
 Query Match 100.0%; Score 64; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00094;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WYDPLTKLML 10
 |||||
 DB 3 WYDPLTKLML 12
 |||||
 RESULT 17
 ABJ00794
 ID ABJ00794 standard; peptide; 14 AA.
 XX
 AC ABJ00794;
 XX

DT 05-SEP-2002 (first entry)
 XX
 DE B lymphocyte affinity maturation library peptide #68.
 XX
 KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW neuropsychiatric; cytostatic; immunostimulant; antitumour; anti-HIV;
 KW antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX
 OS Unidentified.
 XX
 PN WO200216411-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-US025850.
 XX
 PR 18-AUG-2000; 2000US-0226700P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
 XX
 DR WPI; 2002-499775/53.
 XX
 PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide.
 XX
 PS Claim 70; Page 215; 387pp; English.
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 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of BlyS binding polypeptide.
 CC The BlyS binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 XX
 SQ Sequence 14 AA;
 XX
 Query Match 100.0%; Score 64; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00094;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WYDPLTKLML 10
 |||||
 DB 3 WYDPLTKLML 12
 |||||
 RESULT 18
 ABJ00821
 ID ABJ00821 standard; peptide; 14 AA.
 XX
 AC ABJ00821;
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE B lymphocyte affinity maturation library peptide #95.
 XX
 KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW

KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neutroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;
KW antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic;
OS Unidentified.
XX
XX WO200216411-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025850.
XX
XX 18-AUG-2000; 2000US-0226700P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Belzer JP, Potter DM, Fleming TL, Rosen CA;
XX
XX WPI; 2002-499775/53.
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XX administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 216; 387pp; English.
XX
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XX amelioration of a disease or disorder associated with: aberrant B
XX lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
XX of haematopoietic origin; or proliferative disease; and reducing, cells
XX inhibiting or stimulating immunoglobulin production, B cell proliferation
XX and graft rejection involving administration of Blys binding polypeptide.
XX The Blys binding polypeptides are used in the treatment, prevention or
XX amelioration of diseases such as immune system diseases, proliferative
XX diseases, diseases of cells of hematopoietic origin, graft rejection,
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX neurodegenerative diseases. The present sequence is a B lymphocyte
XX stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
|||
3 WYDPLTKLML 12
DB

RESULT 19
ABJ00832
ID ABJ00832 standard; peptide; 14 AA.
XX
XX ABJ00832;
XX
XX 05-SEP-2002 (first entry)
XX
XX B lymphocyte affinity maturation library peptide #106.
XX
XX B lymphocyte stimulator protein binding protein, Blys; immune disease;
XX allergy; proliferative disease; infectious disease; arteriosclerosis;
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX ischaemia; graft-versus-host disease; neurodegenerative disease;
XX immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
XX neutroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;
XX antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic;
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
XX antidiabetic; antithyroid; antidepressant; hepatotropic.
XX

OS Unidentified.
XX
XX WO200216411-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025850.
XX
XX 18-AUG-2000; 2000US-0226700P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Belzer JP, Potter DM, Fleming TL, Rosen CA;
XX
XX WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 216; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
XX amelioration of a disease or disorder associated with: aberrant B
XX lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
XX of haematopoietic origin; or proliferative disease; and reducing, cells
XX inhibiting or stimulating immunoglobulin production, B cell proliferation
XX and graft rejection involving administration of Blys binding polypeptide.
XX The Blys binding polypeptides are used in the treatment, prevention or
XX amelioration of diseases such as immune system diseases, proliferative
XX diseases, diseases of cells of hematopoietic origin, graft rejection,
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX neurodegenerative diseases. The present sequence is a B lymphocyte
XX stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
|||
3 WYDPLTKLML 12
DB

RESULT 20
ABJ00731
ID ABJ00731 standard; peptide; 14 AA.
XX
XX ABJ00731;
XX
XX 05-SEP-2002 (first entry)
XX
XX B lymphocyte affinity maturation library peptide #5.
XX
XX B lymphocyte stimulator protein binding protein, Blys; immune disease;
XX allergy; proliferative disease; infectious disease; arteriosclerosis;
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX ischaemia; graft-versus-host disease; neurodegenerative disease;
XX immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
XX neutroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;
XX antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic;
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
XX antidiabetic; antithyroid; antidepressant; hepatotropic.
OS Unidentified.
XX
XX WO200216411-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025850.
XX

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XX 18-AUG-2000; 2000US-0226700P.
PR (HUMA-) HUMAN GENOME SCT INC.
XX
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 214; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
XX amelioration of a disease or disorder associated with: aberrant B
XX lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
XX of haematopoietic origin; or proliferative disease; and reducing
XX inhibiting or stimulating immunoglobulin production, B cell proliferation
XX and graft rejection involving administration of BlyS binding polypeptide.
XX The BlyS binding polypeptides are used in the treatment, prevention or
XX amelioration of diseases such as immune system diseases, proliferative
XX diseases, diseases of cells of hematopoietic origin, graft rejection,
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX neurodegenerative diseases. The present sequence is a B lymphocyte
XX stimulator protein binding peptide
XX
XX Sequence 14 AA:
SQ
XX
XX Query Match 100.0%; Score 64; DB 5; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 0.00094;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WYDPLTKLWL 10
XX |||||||
XX 3 WYDPLTKLWL 12
DB
XX
XX RESULT 21
XX ABJ00773
XX ID ABJ00773 standard; peptide; 14 AA.
XX AC ABJ00773;
XX
XX 05-SEP-2002 (first entry)
XX
XX B lymphocyte affinity maturation library peptide #47.
XX
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
XX allergy; proliferative disease; infectious disease; arteriosclerosis;
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX ischaemia; graft-versus-host disease; neurodegenerative disease;
XX immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
XX neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;
XX antiasthmatic; anti-allergic; thymostimetic; antianaemic; haemostatic;
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
XX antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX Unidentified.
XX
XX WO200216411-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025850.
XX
XX 18-AUG-2000; 2000US-0226700P.
XX
XX (HUMA-) HUMAN GENOME SCT INC.
XX
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
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DR WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 215; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
XX amelioration of a disease or disorder associated with: aberrant B
XX lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
XX of haematopoietic origin; or proliferative disease; and reducing
XX inhibiting or stimulating immunoglobulin production, B cell proliferation
XX and graft rejection involving administration of BlyS binding polypeptide.
XX The BlyS binding polypeptides are used in the treatment, prevention or
XX amelioration of diseases such as immune system diseases, proliferative
XX diseases, diseases of cells of hematopoietic origin, graft rejection,
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX neurodegenerative diseases. The present sequence is a B lymphocyte
XX stimulator protein binding peptide
XX
XX Sequence 14 AA:
SQ
XX
XX Query Match 100.0%; Score 64; DB 5; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 0.00094;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WYDPLTKLWL 10
XX |||||||
XX 3 WYDPLTKLWL 12
DB
XX
XX RESULT 22
XX ABJ00809
XX ID ABJ00809 standard; peptide; 14 AA.
XX AC ABJ00809;
XX
XX 05-SEP-2002 (first entry)
XX
XX B lymphocyte affinity maturation library peptide #83.
XX
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
XX allergy; proliferative disease; infectious disease; arteriosclerosis;
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX ischaemia; graft-versus-host disease; neurodegenerative disease;
XX immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
XX neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;
XX antiasthmatic; anti-allergic; thymostimetic; antianaemic; haemostatic;
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
XX antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX Unidentified.
XX
XX WO200216411-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025850.
XX
XX 18-AUG-2000; 2000US-0226700P.
XX
XX (HUMA-) HUMAN GENOME SCT INC.
XX
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
XX WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 215; 387pp; English.
XX

```

CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide

SO Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
|||
3 WYDPLTKLML 12

Db

RESULT 23
ABJ00816
ID ABJ00816 standard; peptide; 14 AA.
AC
XX ABJ00816;
XX
XX 05-SEP-2002 (first entry)
XX
XX B lymphocyte affinity maturation library peptide #90.
DE
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thymostimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
KM
XX
XX Unidentified.
OS
XX
XX WO200216411-A2.
PN
XX
XX 28-FEB-2002.
PD
XX
XX 17-AUG-2001; 2001WO-US025850.
PF
XX
XX 18-AUG-2000; 2000US-0226700P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;
PI
XX
XX WPI; 2002-499775/53.
DR
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
PT
XX
XX Claim 70; Page 215; 387pp; English.
PS
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XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide

CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide

SO Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
|||
3 WYDPLTKLML 12

Db

RESULT 24
ABJ00822
ID ABJ00822 standard; peptide; 14 AA.
AC
XX ABJ00822;
XX
XX 05-SEP-2002 (first entry)
XX
XX B lymphocyte affinity maturation library peptide #96.
DE
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thymostimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
KM
XX
XX Unidentified.
OS
XX
XX WO200216411-A2.
PN
XX
XX 28-FEB-2002.
PD
XX
XX 17-AUG-2001; 2001WO-US025850.
PF
XX
XX 18-AUG-2000; 2000US-0226700P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;
PI
XX
XX WPI; 2002-499775/53.
DR
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
PT
XX
XX Claim 70; Page 216; 387pp; English.
PS
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XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide

SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLML 10
3 WYDPLTKLML 12
Db 3 WYDPLTKLML 12
RESULT 25
ABJ00830
ID ABJ00830 standard; peptide; 14 AA.
XX
AC ABJ00830;
XX
DT 05-SEP-2002 (first entry)
XX
DE B lymphocyte affinity maturation library peptide #104.
XX
KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antinaemic; haemostatic;
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
PN WO200216411-A2.
XX
PD 28-FEB-2002.
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PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
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XX
PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
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PI WPI; 2002-499775/53.
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CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing;
CC inhibiting or stimulating immunoglobulin production; B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
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CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLML 10
3 WYDPLTKLML 12

Db 3 WYDPLTKLML 12
RESULT 26
ABJ00831
ID ABJ00831 standard; peptide; 14 AA.
XX
AC ABJ00831;
XX
DT 05-SEP-2002 (first entry)
XX
DE B lymphocyte affinity maturation library peptide #105.
XX
KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antinaemic; haemostatic;
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
PN WO200216411-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
XX
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PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
PI WPI; 2002-499775/53.
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XX
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CC inhibiting or stimulating immunoglobulin production; B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
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CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLML 10
3 WYDPLTKLML 12
Db 3 WYDPLTKLML 12
RESULT 27
ABJ00730
ID ABJ00730 standard; peptide; 14 AA.

XX AC ABJ00730;
XX XX 05-SEP-2002 (first entry)
DE B lymphocyte affinity maturation library peptide #4.
XX B lymphocyte stimulator protein binding protein, BlyS; immune disease;
XX allergy; proliferative disease; infectious disease; arteriosclerosis;
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX ischaemia; graft-versus-host disease; neurodegenerative disease;
XX immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
XX neuromuscular; cytosolic; immunostimulant; antitumour; anti-HIV;
XX antiaesthetic; antiallergic; thymimetic; antineoplastic; haemostatic;
XX dermatologic; antineoplastic; cardiac; ophthalmological; uropathic;
XX antidiabetic; antihypertensive; antidepressant; hepatotropic.
OS Unidentified.
XX WO200216411-A2.
XX PD 28-FEB-2002.
XX PF 17-AUG-2001; 2001WO-US025850.
XX PR 18-AUG-2000; 2000US-0226700P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX PI Belzer JP, Potter DM, Fleming TL, Rosen CA;
XX WPI; 2002-499775/53.
DR The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX PS Claim 70; Page 214; 387pp; English.
XX The present invention relates to the treatment, prevention or
XX amelioration of a disease or disorder associated with: aberrant B
XX lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
XX of haematopoietic origin; or proliferative disease; and reducing,
XX inhibiting or stimulating immunoglobulin production, B cell proliferation
XX and graft rejection involving administration of BlyS binding polypeptide.
XX The BlyS binding polypeptides are used in the treatment, prevention or
XX amelioration of diseases such as immune system diseases, proliferative
XX diseases, diseases of cells of haematopoietic origin, graft rejection,
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX neurodegenerative diseases. The present sequence is a B lymphocyte
XX stimulator protein binding peptide
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKML 10
DB 3 WYDPLTKML 12
RESULT 28
ID ABJ00738 standard; peptide; 14 AA.
XX AC ABJ00738;
XX DT 05-SEP-2002 (first entry)
DE B lymphocyte affinity maturation library peptide #12.

KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuromuscular; cytosolic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thymimetic; antineoplastic; haemostatic;
KW dermatologic; antineoplastic; cardiac; ophthalmological; uropathic;
KW antidiabetic; antihypertensive; antidepressant; hepatotropic.
OS Unidentified.
XX WO200216411-A2.
XX PD 28-FEB-2002.
XX PF 17-AUG-2001; 2001WO-US025850.
XX PR 18-AUG-2000; 2000US-0226700P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX PI Belzer JP, Potter DM, Fleming TL, Rosen CA;
XX WPI; 2002-499775/53.
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XX PS Claim 70; Page 214; 387pp; English.
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XX amelioration of a disease or disorder associated with: aberrant B
XX lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
XX of haematopoietic origin; or proliferative disease; and reducing,
XX inhibiting or stimulating immunoglobulin production, B cell proliferation
XX and graft rejection involving administration of BlyS binding polypeptide.
XX The BlyS binding polypeptides are used in the treatment, prevention or
XX amelioration of diseases such as immune system diseases, proliferative
XX diseases, diseases of cells of haematopoietic origin, graft rejection,
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX neurodegenerative diseases. The present sequence is a B lymphocyte
XX stimulator protein binding peptide
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKML 10
DB 3 WYDPLTKML 12
RESULT 29
ID ABJ00754 standard; peptide; 14 AA.
XX AC ABJ00754;
XX DT 05-SEP-2002 (first entry)
DE B lymphocyte affinity maturation library peptide #28.
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuromuscular; cytosolic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thymimetic; antineoplastic; haemostatic;

KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KM antidiabetic; antithyroid; antidepressant; hepatotropic.
XX Unidentified.
OS
XX WO200216411-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025850.
XX
XX 18-AUG-2000; 2000US-0226700P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;
PI WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 214; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing;
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WYDPLTKLWL 10
|||
3 WYDPLTKLWL 12
DB
RESULT 30
ABJ00777
ID ABJ00777 standard; peptide; 14 AA.
XX
XX ABJ00777;
AC
XX
XX 05-SEP-2002 (first entry)
DT
XX
XX B lymphocyte affinity maturation library peptide #51.
DE
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
KM allergy; proliferative disease; infectious disease; arteriosclerosis;
KM inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KM ischaemia; graft-versus-host disease; neurodegenerative disease;
KM immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KM neutroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KM antiaschematic; antiallergic; thyromimetic; antianaemic; haemostatic;
KM dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KM antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX Unidentified.
OS
XX
XX 18-AUG-2000; 2000US-0226700P.
XX
XX WO200216411-A2.
XX

PD 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025850.
XX
XX 18-AUG-2000; 2000US-0226700P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;
PI WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 215; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing;
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WYDPLTKLWL 10
|||
3 WYDPLTKLWL 12
DB
RESULT 31
ABJ00835
ID ABJ00835 standard; peptide; 14 AA.
XX
XX ABJ00835;
AC
XX
XX 05-SEP-2002 (first entry)
DT
XX
XX B lymphocyte affinity maturation library peptide #109.
DE
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
KM allergy; proliferative disease; infectious disease; arteriosclerosis;
KM inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KM ischaemia; graft-versus-host disease; neurodegenerative disease;
KM immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KM neutroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KM antiaschematic; antiallergic; thyromimetic; antianaemic; haemostatic;
KM dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KM antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX Unidentified.
OS
XX
XX WO200216411-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025850.
XX
XX 18-AUG-2000; 2000US-0226700P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX

XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX DR WPI; 2002-499775/53.
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
PS Claim 70; Page 216; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLML 10
Db 3 WYDPLTKLML 12
RESULT 32
ABJ00771 standard; peptide; 14 AA.
XX AC ABJ00771;
XX DT 05-SEP-2002 (first entry)
XX
XX B lymphocyte affinity maturation library peptide #45.
XX
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytosstatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antinaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX Unidentified.
OS
XX WO200216411-A2.
PN
XX 28-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-US025850.
PP
XX 18-AUG-2000; 2000US-0226700P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
PI
XX WPI; 2002-499775/53.
DR
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.

XX PS Claim 70; Page 215; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLML 10
Db 3 WYDPLTKLML 12
RESULT 33
ABJ00798 standard; peptide; 14 AA.
XX AC ABJ00798;
XX DT 05-SEP-2002 (first entry)
XX
XX B lymphocyte affinity maturation library peptide #72.
XX
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytosstatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antinaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX Unidentified.
OS
XX WO200216411-A2.
PN
XX 28-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-US025850.
PP
XX 18-AUG-2000; 2000US-0226700P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
PI
XX WPI; 2002-499775/53.
DR
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 215; 387pp; English.
PS
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,

CC inhibiting or stimulating immunoglobulin production. B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLML 10
DB 3 WYDPLTKLML 12
RESULT 34
ID ABJ00803 standard; peptide; 14 AA.
XX
AC ABJ00803;
XX
DT 05-SEP-2002 (first entry)
XX
DE B lymphocyte affinity maturation library peptide #77.
XX
KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;
KW antidiabetic; antiallergic; thyromimetic; antinaemic; haemostatic;
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
PN WO200216411-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Belzer JP, Potter DM, Fleming TL, Rosen CA;
XX
PI WPI; 2002-499775/53.
XX
PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.
XX
PS Claim 70; Page 215; 387pp; English.
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CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of hematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinemia, blood clotting disorders, ischaemia, and

CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLML 10
DB 3 WYDPLTKLML 12
RESULT 35
ID ABJ00827 standard; peptide; 14 AA.
XX
AC ABJ00827;
XX
DT 05-SEP-2002 (first entry)
XX
DE B lymphocyte affinity maturation library peptide #101.
XX
KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;
KW antidiabetic; antiallergic; thyromimetic; antinaemic; haemostatic;
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
PN WO200216411-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Belzer JP, Potter DM, Fleming TL, Rosen CA;
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PI WPI; 2002-499775/53.
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XX administering B lymphocyte stimulator binding polypeptide.
XX
PS Claim 70; Page 216; 387pp; English.
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CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of hematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
| | | | | | | | | |
DB 3 WYDPLTKLML 12

RESULT 36
ABJ00833
ID ABJ00833 standard; peptide; 14 AA.
XX
AC ABJ00833;
XX
DT 05-SEP-2002 (first entry)
XX
DE B lymphocyte affinity maturation library peptide #107.
XX
KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;
KW antiaslathmic; anti-allergic; thymometric; antinaemic; haemostatic;
KW dermatological; antinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
PN WO200216411-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Belzter JP, Potter DM, Fleming TL, Rosen CA;
XX
DR WPI; 2002-499775/53.
XX
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PT administering B lymphocyte stimulator binding polypeptide.
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PS Claim 70; Page 216; 387pp; English.
XX
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CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
| | | | | | | | | |
DB 3 WYDPLTKLML 12

RESULT 37
ABJ00737
ID ABJ00737 standard; peptide; 14 AA.
XX
AC ABJ00737;
XX
DT 05-SEP-2002 (first entry)
XX
DE B lymphocyte affinity maturation library peptide #11.
XX
KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;
KW antiaslathmic; anti-allergic; thymometric; antinaemic; haemostatic;
KW dermatological; antinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
PN WO200216411-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Belzter JP, Potter DM, Fleming TL, Rosen CA;
XX
DR WPI; 2002-499775/53.
XX
PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX
PS Claim 70; Page 214; 387pp; English.
XX
CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
| | | | | | | | | |
DB 3 WYDPLTKLML 12

RESULT 38
ABJ00740
ID ABJ00740 standard; peptide; 14 AA.
XX
AC ABJ00740;
XX
DT 05-SEP-2002 (first entry)


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XX XX WO200216411-A2.
XX PN
XX XX
XX PD 28-FEB-2002.
XX PF 17-AUG-2001; 2001WO-US025850.
XX XX
XX PR 18-AUG-2000; 2000US-0226700P.
XX XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX PS WPI; 2002-499775/53.
XX XX
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX PT administering B lymphocyte stimulator binding polypeptide.
XX XX
XX PS Claim 70; Page 215; 387pp; English.
XX XX
XX CC The present invention relates to the treatment, prevention or
XX CC amelioration of a disease or disorder associated with: aberrant B
XX CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
XX CC of haematopoietic origin; or proliferative disease; and reducing,
XX CC inhibiting or stimulating immunoglobulin production, B cell proliferation
XX CC and graft rejection involving administration of Blys binding polypeptide.
XX CC The Blys binding polypeptides are used in the treatment, prevention or
XX CC amelioration of diseases such as immune system diseases, proliferative
XX CC diseases, diseases of cells of haematopoietic origin, graft rejection,
XX CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX CC neurodegenerative diseases. The present sequence is a B lymphocyte
XX CC stimulator protein binding peptide
XX XX
XX SQ Sequence 14 AA;
XX XX
XX Query Match 100.0%; Score 64; DB 5; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 0.00094;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
QY 1 WYDPLTKLML 10
XX |||||
XX Db 3 WYDPLTKLML 12
XX
XX RESULT 41
XX ABJ00802
XX ID ABJ00802 standard; peptide; 14 AA.
XX XX
XX AC ABJ00802;
XX XX
XX DT 05-SEP-2002 (first entry)
XX XX
XX DE B lymphocyte affinity maturation library peptide #76.
XX XX
XX KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
XX KW allergy; proliferative disease; infectious disease; arteriosclerosis;
XX KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX KW ischaemia; graft-versus-host disease; neurodegenerative disease;
XX KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
XX KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
XX KW antiaesthetic; anti-allergic; thymimetic; antanaemic; haemostatic;
XX KW dermatological; antiinflammatory; cardiant; opthalmological; uropathic;
XX KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX XX
XX OS Unidentified.
XX XX
XX PN WO200216411-A2.
XX XX
XX PD 28-FEB-2002.
XX XX
XX PI 17-AUG-2001; 2001WO-US025850.
XX PF
XX PR
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX PS WPI; 2002-499775/53.
XX XX

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PR 18-AUG-2000; 2000US-0226700P.
XX XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX XX
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX XX
XX DR WPI; 2002-499775/53.
XX XX
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX PT administering B lymphocyte stimulator binding polypeptide.
XX XX
XX PS Claim 70; Page 215; 387pp; English.
XX XX
XX CC The present invention relates to the treatment, prevention or
XX CC amelioration of a disease or disorder associated with: aberrant B
XX CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
XX CC of haematopoietic origin; or proliferative disease; and reducing,
XX CC inhibiting or stimulating immunoglobulin production, B cell proliferation
XX CC and graft rejection involving administration of Blys binding polypeptide.
XX CC The Blys binding polypeptides are used in the treatment, prevention or
XX CC amelioration of diseases such as immune system diseases, proliferative
XX CC diseases, diseases of cells of haematopoietic origin, graft rejection,
XX CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX CC neurodegenerative diseases. The present sequence is a B lymphocyte
XX CC stimulator protein binding peptide
XX XX
XX SQ Sequence 14 AA;
XX XX
XX Query Match 100.0%; Score 64; DB 5; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 0.00094;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
QY 1 WYDPLTKLML 10
XX |||||
XX Db 3 WYDPLTKLML 12
XX
XX RESULT 42
XX ABJ00815
XX ID ABJ00815 standard; peptide; 14 AA.
XX XX
XX AC ABJ00815;
XX XX
XX DT 05-SEP-2002 (first entry)
XX XX
XX DE B lymphocyte affinity maturation library peptide #89.
XX XX
XX KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
XX KW allergy; proliferative disease; infectious disease; arteriosclerosis;
XX KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX KW ischaemia; graft-versus-host disease; neurodegenerative disease;
XX KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
XX KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
XX KW antiaesthetic; anti-allergic; thymimetic; antanaemic; haemostatic;
XX KW dermatological; antiinflammatory; cardiant; opthalmological; uropathic;
XX KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX XX
XX OS Unidentified.
XX XX
XX PN WO200216411-A2.
XX XX
XX PD 28-FEB-2002.
XX XX
XX PF 17-AUG-2001; 2001WO-US025850.
XX PR
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX PS WPI; 2002-499775/53.
XX XX

```

XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B Lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 215; 387pp; English.
PS
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, graft rejection,
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
|||
3 WYDPLTKLML 12
Db

RESULT 43
ABJ00829 standard; peptide; 14 AA.
ID
AC ABJ00829;
XX
XX 05-SEP-2002 (first entry)
DT
DE B lymphocyte affinity maturation library peptide #103.
XX
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaschematic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX Unidentified.
OS
XX WO200216411-A2.
PN
XX 28-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-US025850.
PF
XX 18-AUG-2000; 2000US-0226700P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
PI
XX WPI; 2002-499775/53.
DR
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B Lymphocyte stimulator binding polypeptide.
XX
PS Claim 70; Page 216; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or

CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, graft rejection,
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
|||
3 WYDPLTKLML 12
Db

RESULT 44
ABJ00729 standard; peptide; 14 AA.
ID
AC ABJ00729;
XX
XX 05-SEP-2002 (first entry)
DT
DE B lymphocyte affinity maturation library peptide #3.
XX
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaschematic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX Unidentified.
OS
XX WO200216411-A2.
PN
XX 28-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-US025850.
PF
XX 18-AUG-2000; 2000US-0226700P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
PI
XX WPI; 2002-499775/53.
DR
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B Lymphocyte stimulator binding polypeptide.
XX
PS Claim 70; Page 214; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative

CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
hypermagmaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
stimulator protein binding peptide

SQ Sequence 14 AA;

Query Match	100.0%;	Score 64;	DB 5;	Length 14;
Best Local Similarity	100.0%;	Pred. No. 0.00094;		
Matches	10;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

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Qy      1 WYDPLTKLWL 10
         |||||
Db      3 WYDPLTKLWL 12

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RESULT 45
ABJ00756
ID   ABJ00756 standard; peptide; 14 AA

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DT 05-SEP-2002 (first entry)

DE B Lymphocyte affinity maturation library peptide #30.

KM lymphocyte stimulator protein binding protein; BVS; immune disease;
KM allergy; proliferative disease; infectious disease; arteriosclerosis;
KM inflammatory disorder; hypergammaglobulinemia; blood clotting;
KM ischaemia; graft-versus-host disease; neurodegenerative disease;
KM immunosuppressive; neutrotropic; antineutrotic; anti-thyroid;
KM neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KM antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic;
KM dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KM antidiabetic; antithyroid; antidepressant; hepatotropic.

Unidentified. OS

PN WO200216411-A2.

PD 28-FEB-2002.

PF 17-AUG-2001; 2001WO-US025850.

PR 18-AUG-2000; 2000US-0226700P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;

DR WPI; 2002-499775/53.

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 214; 387pp; English

The present invention relates to the treatment, prevention or amelioration of a disease or disorder associated with aberrant B lymphocyte stimulator (Blys), Blys receptor expression or activity; cells of hematopoietic origin; or proliferative disease; and reducing, inhibiting or stimulating immunoglobulin production, B cell proliferation and graft rejection involving administration of Blys binding polypeptide. The Blys binding polypeptides are used in the treatment, prevention or amelioration of diseases such as immune system diseases, proliferative diseases, diseases of cells of hematopoietic origin, graft rejection, allergies, infectious diseases, arteriosclerosis, inflammatory disorders, hypergammaglobulinaemia, blood clotting disorders, ischaemia, and neurodegenerative diseases. The present sequence is a B lymphocyte stimulator protein binding peptide

50 Sequence 14 AA:

Query Match	100.0%;	Score 64;	DB 5;	Length 14;
Best Local Similarity	100.0%;	Pred. No. 0.00094;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	WYDPLTKLWL	10
Db	3	WYDPLTKLWL	12

RESULT 46
ABJ00785
ID ABJ00785 standard; peptide; 14 AA

AC ABJ00785;

DE B Lymphocyte affinity maturation library peptide #59.

KM lymphocyte stimulator protein binding protein; BvS; immune disease;
KM allergy; proliferative disease; infectious disease; arteriosclerosis;
KM inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KM ischaemia; graft-versus-host disease; neurodegenerative disease;
KM immunosuppressive; nephrotropic; antineumatic; antiarthritic;
KM neuroprotective; cytostatic; immunostimulant; anti-HIV;
KM antiaesthetic; antiallergic; thyromimetic; antianemic; hemostatic;
KM dermatological; antihistaminergic; cardiant; ophthalmotologic; uropathic;
KM antidiabetic; antithyroid; antidepressant; hepatocellular;

OS Unidentified.

PN WO200216411-A2.

PD 28-FEB-2002.

PF 17-AUG-2001; 2001WO-US025850.

PR 18-AUG-2000; 2000US-0226700P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;

DR WPI; 2002-499775/53.

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises administering B lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 215; 387pp; English

The present invention relates to the treatment/prevention or amelioration of a disease or disorder associated with: aberrant B lymphocyte stimulator (Blys), Blys receptor expression or activity; cells of hematopoietic origin; or proliferative disease; and reducing, inhibiting or stimulating immunoglobulin production, B cell proliferation and graft rejection involving administration of Blys binding polypeptide. The Blys binding polypeptides are used in the treatment, prevention or amelioration of diseases such as immune system diseases, proliferative diseases, diseases of cells of hematopoietic origin, graft rejection, allergies, infectious diseases, arteriosclerosis, inflammatory disorders, hypercycmaglobulinaemia, blood clotting disorders, ischaemia, and neurodegenerative diseases. The present sequence is a B lymphocyte stimulator protein binding peptide.

SQ Sequence 14 AA;

Query Match	100.0%;	Score 64;	DB 5;	Length 14;
Best Local Similarity	100.0%;	Pred. No. 0.00094;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 1 WYDPLTKLWL 10
|||||||

Db 3 WYDPLTKLML 12

RESULT 47

ABJ00790 standard; peptide; 14 AA.

AC ABJ00790;

DT 05-SEP-2002 (first entry)

B lymphocyte affinity maturation library peptide #64.

B lymphocyte stimulator protein binding protein; BlyS; immune disease; allergy; proliferative disease; infectious disease; arteriosclerosis; inflammatory disorder; hypergammaglobulinaemia; blood clotting; ischaemia; graft-versus-host disease; neurodegenerative disease; immunosuppressive; nephrotropic; antirheumatic; antitumour; anti-HIV; neuropsychiatric; cytosolic; immunostimulant; antianemic; haemostatic; antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic; dermatological; antiinflammatory; cardiac; ophthalmological; uropathic; antidiabetic; antithyroid; antidepressant; hepatotropic.

OS Unidentified.

PN WO200216411-A2.

PD 28-FEB-2002.

PF 17-AUG-2001; 2001WO-US025850.

PR 18-AUG-2000; 2000US-0226700P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Belzer JP, Potter DM, Fleming TL, Rosen CA;

DR WPI; 2002-499775/53.

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises administering B lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 215; 387pp; English.

CC The present invention relates to the treatment, prevention or amelioration of a disease or disorder associated with: aberrant B lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells of haematopoietic origin; or proliferative disease; and reducing, inhibiting or stimulating immunoglobulin production, B cell proliferation and graft rejection involving administration of BlyS binding polypeptide. The BlyS binding polypeptides are used in the treatment, prevention or amelioration of diseases such as immune system diseases, proliferative diseases, diseases of cells of haematopoietic origin, graft rejection, allergies, infectious diseases, arteriosclerosis, inflammatory disorders, hypergammaglobulinaemia, blood clotting disorders, ischaemia, and neurodegenerative diseases. The present sequence is a B lymphocyte stimulator protein binding peptide

SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00094; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10

Db 3 WYDPLTKLML 12

RESULT 48
ABJ00792
ID ABJ00792 standard; peptide; 14 AA.

AC ABJ00792;

DT 05-SEP-2002 (first entry)

B lymphocyte affinity maturation library peptide #64.

B lymphocyte stimulator protein binding protein; BlyS; immune disease; allergy; proliferative disease; infectious disease; arteriosclerosis; inflammatory disorder; hypergammaglobulinaemia; blood clotting; ischaemia; graft-versus-host disease; neurodegenerative disease; immunosuppressive; nephrotropic; antirheumatic; antitumour; anti-HIV; neuropsychiatric; cytosolic; immunostimulant; antianemic; haemostatic; antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic; dermatological; antiinflammatory; cardiac; ophthalmological; uropathic; antidiabetic; antithyroid; antidepressant; hepatotropic.

OS Unidentified.

PN WO200216411-A2.

PD 28-FEB-2002.

PF 17-AUG-2001; 2001WO-US025850.

PR 18-AUG-2000; 2000US-0226700P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Belzer JP, Potter DM, Fleming TL, Rosen CA;

DR WPI; 2002-499775/53.

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises administering B lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 215; 387pp; English.

CC The present invention relates to the treatment, prevention or amelioration of a disease or disorder associated with: aberrant B lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells of haematopoietic origin; or proliferative disease; and reducing, inhibiting or stimulating immunoglobulin production, B cell proliferation and graft rejection involving administration of BlyS binding polypeptide. The BlyS binding polypeptides are used in the treatment, prevention or amelioration of diseases such as immune system diseases, proliferative diseases, diseases of cells of haematopoietic origin, graft rejection, allergies, infectious diseases, arteriosclerosis, inflammatory disorders, hypergammaglobulinaemia, blood clotting disorders, ischaemia, and neurodegenerative diseases. The present sequence is a B lymphocyte stimulator protein binding peptide

SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00094; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10

Db 3 WYDPLTKLML 12

RESULT 49
ABJ00732
ID ABJ00732 standard; peptide; 14 AA.

AC ABJ00732;

DT 05-SEP-2002 (first entry)

B lymphocyte affinity maturation library peptide #6.

B lymphocyte stimulator protein binding protein; BlyS; immune disease;

KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;
 KW antiaesthetic; antiallergic; thymostatic; antianemic; haemostatic;
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX
 OS Unidentified.
 XX
 PN WO200216411-A2.
 XX
 PD 28-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-US025850.
 XX
 PF 18-AUG-2000; 2000US-0226700P.
 XX
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA Beltzer JP, Potter DM, Fleming TL, Rosen CA;
 XX
 PI WPI; 2002-499775/53.
 XX
 DR The treatment of various diseases e.g. rheumatoid arthritis, comprises
 XX administering B lymphocyte stimulator binding polypeptide.
 PT
 XX Claim 70; Page 214; 387PP; English.
 XX
 PS The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of Blys binding polypeptide.
 CC The Blys binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 CC
 XX Sequence 14 AA;
 SQ
 Query Match 100.0%; Score 64; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00094;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WYDPLTKLWL 10
 |||||||||
 Db 3 WYDPLTKLWL 12
 RESULT 50
 ABJ00742 standard; peptide; 14 AA.
 ID
 AC ABJ00742;
 XX
 XX 05-SEP-2002 (first entry)
 DT
 XX B lymphocyte affinity maturation library peptide #16.
 DE
 XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;
 KW antiaesthetic; antiallergic; thymostatic; antianemic; haemostatic;
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;

KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX
 OS Unidentified.
 XX
 PN WO200216411-A2.
 XX
 PD 28-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-US025850.
 XX
 PF 18-AUG-2000; 2000US-0226700P.
 XX
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA Beltzer JP, Potter DM, Fleming TL, Rosen CA;
 XX
 PI WPI; 2002-499775/53.
 XX
 DR The treatment of various diseases e.g. rheumatoid arthritis, comprises
 XX administering B lymphocyte stimulator binding polypeptide.
 PT
 XX Claim 70; Page 214; 387PP; English.
 XX
 PS The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of Blys binding polypeptide.
 CC The Blys binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 CC
 XX Sequence 14 AA;
 SQ
 Query Match 100.0%; Score 64; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00094;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WYDPLTKLWL 10
 |||||||||
 Db 3 WYDPLTKLWL 12
 RESULT 51
 ABJ00757 standard; peptide; 14 AA.
 ID
 AC ABJ00757;
 XX
 XX 05-SEP-2002 (first entry)
 DT
 XX B lymphocyte affinity maturation library peptide #31.
 DE
 XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;
 KW antiaesthetic; antiallergic; thymostatic; antianemic; haemostatic;
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX
 OS Unidentified.
 XX
 PN WO200216411-A2.
 XX
 PD 28-FEB-2002.

XX 17-AUG-2001; 2001WO-US025850.
PF 18-AUG-2000; 2000US-0226700P.
PR (HUMA-) HUMAN GENOME SCI INC.
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX WPI; 2002-499775/53.
DR
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 214; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WYDPLTKLML 10
 |||||
 3 WYDPLTKLML 12
DB
RESULT 52
ABJ00758
ID ABJ00758 standard; peptide; 14 AA.
XX
XX ABJ00758;
AC
XX
XX 05-SEP-2002 (first entry)
DT
XX
XX B lymphocyte affinity maturation library peptide #32.
DE
XX
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thymometric; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
KW
XX
XX unidentified.
OS
XX
XX WO200216411-A2.
PN
XX
XX 28-FEB-2002.
PD
XX
XX 17-AUG-2001; 2001WO-US025850.
PF
XX
XX 18-AUG-2000; 2000US-0226700P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX

PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX WPI; 2002-499775/53.
DR
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 214; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WYDPLTKLML 10
 |||||
 3 WYDPLTKLML 12
DB
RESULT 53
ABJ00761
ID ABJ00761 standard; peptide; 14 AA.
XX
XX ABJ00761;
AC
XX
XX 05-SEP-2002 (first entry)
DT
XX
XX B lymphocyte affinity maturation library peptide #35.
DE
XX
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thymometric; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
KW
XX
XX unidentified.
OS
XX
XX WO200216411-A2.
PN
XX
XX 28-FEB-2002.
PD
XX
XX 17-AUG-2001; 2001WO-US025850.
PF
XX
XX 18-AUG-2000; 2000US-0226700P.
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CC stimulator protein binding peptide

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Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10
3 WYDPLTKLML 12

Db

RESULT 54

ABJ00769 standard; peptide; 14 AA.

XX ABJ00769;

AC

XX 05-SEP-2002 (first entry)

DT

DE B lymphocyte affinity maturation library peptide #43.

XX

XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX

OS unidentified.

XX

XX WO200216411-A2.

PN

XX 28-FEB-2002.

PD

XX 17-AUG-2001; 2001WO-US025850.

PF

XX 18-AUG-2000; 2000US-0226700P.

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CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide

CC and graft rejection involving administration of Blys binding polypeptide.

CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
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CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide

SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10
3 WYDPLTKLML 12

Db

RESULT 55

ABJ00780 standard; peptide; 14 AA.

XX ABJ00780;

AC

XX 05-SEP-2002 (first entry)

DT

DE B lymphocyte affinity maturation library peptide #54.

XX

XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX

OS unidentified.

XX

XX WO200216411-A2.

PN

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CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide

ABJ00806
ID ABJ00806 standard; peptide; 14 AA.
XX
AC ABJ00806;
XX
DT 05-SEP-2002 (first entry)
XX
DE B lymphocyte affinity maturation library peptide #80.
XX
KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;
KW neutrophilic; cytostatic; immunostimulant; antitumor; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
FN WO200216411-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
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DR WPI; 2002-499775/53.
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CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
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CC diseases, diseases of cells of hematopoietic origin, graft rejection,
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CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;
XX
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLML 10
DB 3 WYDPLTKLML 12
XX
RESULT 59
ABJ00817
ID ABJ00817 standard; peptide; 14 AA.
XX
AC ABJ00817;
XX
DT 05-SEP-2002 (first entry)
XX

DE B lymphocyte affinity maturation library peptide #91.
XX
KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;
KW neutrophilic; cytostatic; immunostimulant; antitumor; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
FN WO200216411-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
XX
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PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
DR WPI; 2002-499775/53.
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PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
PR administering B lymphocyte stimulator binding polypeptide.
XX
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CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;
XX
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLML 10
DB 3 WYDPLTKLML 12
XX
RESULT 60
ABJ00752
ID ABJ00752 standard; peptide; 14 AA.
XX
AC ABJ00752;
XX
DT 05-SEP-2002 (first entry)
XX
DE B lymphocyte affinity maturation library peptide #26.
XX
KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;
KW

XX (HUMA-) HUMAN GENOME SCI INC.
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;
XX WPI; 2002-499775/53.
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PT administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 215; 387pp; English.
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CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
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CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
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CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLML 10
Db 3 WYDPLTKLML 12
RESULT 63
ABU00735 100.0%; Score 64; DB 5; Length 14;
ID ABU00735 standard; peptide; 14 AA.
AC ABU00735;
XX
XX 05-SEP-2002 (first entry)
DT
DE B lymphocyte affinity maturation library peptide #9.
XX
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cycostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX Unidentified.
OS
XX WO200216411-A2.
PN
XX 28-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-US025850.
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CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
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CC and graft rejection involving administration of Blys binding polypeptide.
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CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLML 10
Db 3 WYDPLTKLML 12
RESULT 64
ABU00736 100.0%; Score 64; DB 5; Length 14;
ID ABU00736 standard; peptide; 14 AA.
AC ABU00736;
XX
XX 05-SEP-2002 (first entry)
DT
DE B lymphocyte affinity maturation library peptide #10.
XX
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cycostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
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XX Unidentified.
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CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
CC
SQ Sequence 14 AA;
QY 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 65
ABJ00749
ID ABJ00749 standard; peptide; 14 AA.
XX
AC ABJ00749;
DT 05-SEP-2002 (first entry)
DE B lymphocyte affinity maturation library peptide #23.
XX
KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;
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KW antiaesthetic; antiallergic; thymometric; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
PN WO200216411-A2.
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PD 28-FEB-2002.
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CC and graft rejection involving administration of Blys binding polypeptide.
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CC hypergammaglobulinemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
CC
SQ Sequence 14 AA;
QY 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 66
ABJ00762
ID ABJ00762 standard; peptide; 14 AA.
XX
AC ABJ00762;
DT 05-SEP-2002 (first entry)
DE B lymphocyte affinity maturation library peptide #36.
XX
KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;
KW antiaesthetic; antiallergic; thymometric; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
PN WO200216411-A2.
XX
PD 28-FEB-2002.
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PF 17-AUG-2001; 2001WO-US025850.
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CC diseases, diseases of cells of hematopoietic origin, graft rejection,
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CC hypergammaglobulinemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
CC
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10
|||
DB 3 WYDPLTKLML 12

RESULT 67

ABJ00766
ID ABJ00766 standard; peptide; 14 AA.

XX AC ABJ00766;

DT 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #40.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
allergy; proliferative disease; infectious disease; arteriosclerosis;
inflammatory disorder; hypergammaglobulinaemia; blood clotting;
ischaemia; graft-versus-host disease; neurodegenerative disease;
immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
antidiabetic; antithyroid; antidepressant; hepatotropic.

XX OS unidentified.

XX PN WO200216411-A2.

XX PD 28-FEB-2002.

XX PF 17-AUG-2001; 2001WO-US025850.

XX PR 18-AUG-2000; 2000US-0226700P.

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XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;

XX DR WPI, 2002-499775/53.

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and graft rejection involving administration of BlyS binding polypeptide.
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amelioration of diseases such as immune system diseases, proliferative
diseases, diseases of cells of haematopoietic origin, graft rejection,
allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
neurodegenerative diseases. The present sequence is a B lymphocyte
stimulator protein binding peptide

XX SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10
|||
DB 3 WYDPLTKLML 12

RESULT 68

ABJ00775
ID ABJ00775 standard; peptide; 14 AA.

XX AC ABJ00775;

DT 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #49.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
allergy; proliferative disease; infectious disease; arteriosclerosis;
inflammatory disorder; hypergammaglobulinaemia; blood clotting;
ischaemia; graft-versus-host disease; neurodegenerative disease;
immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
antidiabetic; antithyroid; antidepressant; hepatotropic.

XX OS unidentified.

XX PN WO200216411-A2.

XX PD 28-FEB-2002.

XX PF 17-AUG-2001; 2001WO-US025850.

XX PR 18-AUG-2000; 2000US-0226700P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;

XX DR WPI, 2002-499775/53.

XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
administering B lymphocyte stimulator binding polypeptide.

XX PS Claim 70; Page 215; 387pp; English.

XX The present invention relates to the treatment, prevention or
amelioration of a disease or disorder associated with: aberrant B
lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
of haematopoietic origin; or proliferative disease; and reducing,
inhibiting or stimulating immunoglobulin production, B cell proliferation
and graft rejection involving administration of BlyS binding polypeptide.
The BlyS binding polypeptides are used in the treatment, prevention or
amelioration of diseases such as immune system diseases, proliferative
diseases, diseases of cells of haematopoietic origin, graft rejection,
allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
neurodegenerative diseases. The present sequence is a B lymphocyte
stimulator protein binding peptide

XX SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10
|||
DB 3 WYDPLTKLML 12

RESULT 69

ABJ00776
ID ABJ00776 standard; peptide; 14 AA.

XX AC ABJ00776;

XX 05-SEP-2002 (first entry)
 DT B lymphocyte affinity maturation library peptide #50.
 XX
 XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW immunoprotective; cytosolic; immunostimulant; antitumour; anti-HIV;
 KW antineoplastic; antiallergic; immunostimulant; antitumour; anti-HIV;
 KW antiasbatic; antiallergic; thymometric; antineoplastic; haemostatic;
 KW dermatological; antineoplastic; antineoplastic; antineoplastic; uropathic;
 KW antidiabetic; antihypertensive; antidepressant; hepatotropic.
 XX
 XX Unidentified.
 XX
 XX WO200216411-A2.
 XX
 XX 28-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-US025850.
 XX
 XX 18-AUG-2000; 2000US-0226700P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
 XX
 XX WPI; 2002-499775/53.
 XX
 XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide.
 XX
 XX Claim 70; Page 215; 387pp; English.
 XX
 XX The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of BlyS binding polypeptide.
 CC The BlyS binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of haematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 CC
 XX Sequence 14 AA:
 SQ
 Query Match 100.0%; Score 64; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00094;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WYDPLTKLML 10
 |||||
 DB 3 WYDPLTKLML 12
 |||||
 RESULT 70
 ABJ00824 standard; peptide; 14 AA.
 ID ABJ00824
 XX
 XX ABJ00824;
 XX
 XX 05-SEP-2002 (first entry)
 DT B lymphocyte affinity maturation library peptide #98.
 XX
 XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW immunoprotective; cytosolic; immunostimulant; antitumour; anti-HIV;
 KW antineoplastic; antiallergic; immunostimulant; antitumour; anti-HIV;
 KW antiasbatic; antiallergic; thymometric; antineoplastic; haemostatic;
 KW dermatological; antineoplastic; antineoplastic; antineoplastic; uropathic;
 KW antidiabetic; antihypertensive; antidepressant; hepatotropic.

KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW immunoprotective; cytosolic; immunostimulant; antitumour; anti-HIV;
 KW antiasbatic; antiallergic; immunostimulant; antitumour; anti-HIV;
 KW dermatological; antineoplastic; antineoplastic; antineoplastic; uropathic;
 KW antidiabetic; antihypertensive; antidepressant; hepatotropic.
 XX
 XX Unidentified.
 XX
 XX WO200216411-A2.
 XX
 XX 28-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-US025850.
 XX
 XX 18-AUG-2000; 2000US-0226700P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
 XX
 XX WPI; 2002-499775/53.
 XX
 XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide.
 XX
 XX Claim 70; Page 216; 387pp; English.
 XX
 XX The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of BlyS binding polypeptide.
 CC The BlyS binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of haematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 CC
 XX Sequence 14 AA:
 SQ
 Query Match 100.0%; Score 64; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00094;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WYDPLTKLML 10
 |||||
 DB 3 WYDPLTKLML 12
 |||||
 RESULT 71
 ABJ00834 standard; peptide; 14 AA.
 ID ABJ00834
 XX
 XX ABJ00834;
 XX
 XX 05-SEP-2002 (first entry)
 DT B lymphocyte affinity maturation library peptide #108.
 XX
 XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW immunoprotective; cytosolic; immunostimulant; antitumour; anti-HIV;
 KW antineoplastic; antiallergic; immunostimulant; antitumour; anti-HIV;
 KW antiasbatic; antiallergic; thymometric; antineoplastic; haemostatic;
 KW dermatological; antineoplastic; antineoplastic; antineoplastic; uropathic;
 KW antidiabetic; antihypertensive; antidepressant; hepatotropic.

XX OS Unidentified.
XX XX WO200216411-A2.
XX PD 28-FEB-2002.
XX PF 17-AUG-2001; 2001WO-US025850.
XX PR 18-AUG-2000; 2000US-0226700P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX DR WPI; 2002-499775/53.
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX PR administering B lymphocyte stimulator binding polypeptide.
XX PS Claim 70; Page 216; 387pp; English.
XX CC The present invention relates to the treatment, prevention or
XX CC amelioration of a disease or disorder associated with: aberrant B
XX CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
XX CC of haematopoietic origin; or proliferative disease; and reducing, cells
XX CC inhibiting or stimulating immunoglobulin production, B cell proliferation
XX CC and graft rejection involving administration of Blys binding polypeptide.
XX CC The Blys binding polypeptides are used in the treatment, prevention or
XX CC amelioration of diseases such as immune system diseases, proliferative
XX CC diseases, infectious diseases of cells of hematopoietic origin, graft rejection,
XX CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX CC neurodegenerative diseases. The present sequence is a B lymphocyte
XX CC stimulator protein binding peptide
XX SQ Sequence 14 AA;
XX
XX Query Match 100.0%; Score 64; DB 5; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 0.00094;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WYDPLTKLML 10
XX |||||
DB 3 WYDPLTKLML 12
RESULT 72
ID ABJ00728 standard; peptide; 14 AA.
XX AC ABJ00728;
XX DT 05-SEP-2002 (first entry)
XX DE B lymphocyte affinity maturation library peptide #2.
XX KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
XX KW allergy; proliferative disease; infectious disease; arteriosclerosis;
XX KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX KW ischaemia; graft-versus-host disease; neurodegenerative disease;
XX KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
XX KW neuroprotective; cytosatic; immunostimulant; antitumor; anti-HIV;
XX KW antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;
XX KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
XX KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX OS Unidentified.
XX XX WO200216411-A2.
XX PD 28-FEB-2002.

PF 17-AUG-2001; 2001WO-US025850.
XX PR 18-AUG-2000; 2000US-0226700P.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX PA Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX PI WPI; 2002-499775/53.
XX DR WPI; 2002-499775/53.
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX PR administering B lymphocyte stimulator binding polypeptide.
XX PS Claim 70; Page 214; 387pp; English.
XX CC The present invention relates to the treatment, prevention or
XX CC amelioration of a disease or disorder associated with: aberrant B
XX CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
XX CC of haematopoietic origin; or proliferative disease; and reducing, cells
XX CC inhibiting or stimulating immunoglobulin production, B cell proliferation
XX CC and graft rejection involving administration of Blys binding polypeptide.
XX CC The Blys binding polypeptides are used in the treatment, prevention or
XX CC amelioration of diseases such as immune system diseases, proliferative
XX CC diseases, infectious diseases of cells of hematopoietic origin, graft rejection,
XX CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX CC neurodegenerative diseases. The present sequence is a B lymphocyte
XX CC stimulator protein binding peptide
XX SQ Sequence 14 AA;
XX
XX Query Match 100.0%; Score 64; DB 5; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 0.00094;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WYDPLTKLML 10
XX |||||
DB 3 WYDPLTKLML 12
RESULT 73
ID ABJ00747 standard; peptide; 14 AA.
XX AC ABJ00747;
XX DT 05-SEP-2002 (first entry)
XX DE B lymphocyte affinity maturation library peptide #21.
XX KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
XX KW allergy; proliferative disease; infectious disease; arteriosclerosis;
XX KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX KW ischaemia; graft-versus-host disease; neurodegenerative disease;
XX KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
XX KW neuroprotective; cytosatic; immunostimulant; antitumor; anti-HIV;
XX KW antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;
XX KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
XX KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX OS Unidentified.
XX XX WO200216411-A2.
XX PD 28-FEB-2002.
XX PF 17-AUG-2001; 2001WO-US025850.
XX PR 18-AUG-2000; 2000US-0226700P.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;

XX WP1; 2002-499775/53.
DR The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.
PT Claim 70; Page 214; 387pp; English.
PS
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
CC
SQ Sequence 14 AA:
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WYDPLTKLWL 10
|||
3 WYDPLTKLWL 12
DB 3 WYDPLTKLWL 12
RESULT 74
ABJ00750
ID ABJ00750 standard; peptide; 14 AA.
XX
AC ABJ00750;
XX
DT 05-SEP-2002 (first entry)
DE
XX B lymphocyte affinity maturation library peptide #24.
DE
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
PN WO200216411-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
XX WP1; 2002-499775/53.
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX
PS Claim 70; Page 214; 387pp; English.

XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
CC
SQ Sequence 14 AA:
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WYDPLTKLWL 10
|||
3 WYDPLTKLWL 12
DB 3 WYDPLTKLWL 12
RESULT 75
ABJ00755
ID ABJ00755 standard; peptide; 14 AA.
XX
AC ABJ00755;
XX
DT 05-SEP-2002 (first entry)
DE
XX B lymphocyte affinity maturation library peptide #29.
DE
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
PN WO200216411-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
XX WP1; 2002-499775/53.
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX
PS Claim 70; Page 214; 387pp; English.
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.

CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12
RESULT 76
ABJ00763 standard; peptide; 14 AA.
XX
AC ABJ00763;
XX
DT 05-SEP-2002 (first entry)
DE B lymphocyte affinity maturation library peptide #37.
XX
KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neutroprotective; cycostatic; immunostimulant; antitumour; anti-HIV;
KW antiasclastic; antiallergic; thymomimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
PN WO200216411-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
DR WPI; 2002-499775/53.
XX
PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX
PS Claim 70; Page 214; 387pp; English.
XX
CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide

XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12
RESULT 77
ABJ00779 standard; peptide; 14 AA.
XX
AC ABJ00779;
XX
DT 05-SEP-2002 (first entry)
DE B lymphocyte affinity maturation library peptide #53.
XX
KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neutroprotective; cycostatic; immunostimulant; antitumour; anti-HIV;
KW antiasclastic; antiallergic; thymomimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
PN WO200216411-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
DR WPI; 2002-499775/53.
XX
PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX
PS Claim 70; Page 215; 387pp; English.
XX
CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
| | | | |
DB 3 WYDPLTKLWL 12

RESULT 78

ID ABJ00825 standard; peptide; 14 AA.

XX ABJ00825;

DT 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #99.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antistimetic; antiallergic; thyromimetic; antinaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

OS Unidentified.

XX MO200216411-A2.

PN 17-AUG-2001; 2001WO-US025850.

XX 28-FEB-2002.

PF 17-AUG-2001; 2001WO-US025850.

XX 18-AUG-2000; 2000US-0226700P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;

XX WPI; 2002-499775/53.

XX The treatment of various diseases e.g. rheumatoid arthritis, comprises

XX administering B lymphocyte stimulator binding polypeptide.

XX Claim 70; Page 216; 387pp; English.

XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
XX stimulator protein binding peptide

XX Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
| | | | |
DB 3 WYDPLTKLWL 12

RESULT 79

ABJ00741

ID ABJ00741 standard; peptide; 14 AA.

XX ABJ00741;

DT 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #15.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antistimetic; antiallergic; thyromimetic; antinaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

OS Unidentified.

XX MO200216411-A2.

PN 17-AUG-2001; 2001WO-US025850.

XX 28-FEB-2002.

PF 17-AUG-2001; 2001WO-US025850.

XX 18-AUG-2000; 2000US-0226700P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;

XX WPI; 2002-499775/53.

XX The treatment of various diseases e.g. rheumatoid arthritis, comprises

XX administering B lymphocyte stimulator binding polypeptide.

XX Claim 70; Page 214; 387pp; English.

XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
XX stimulator protein binding peptide

XX Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
| | | | |
DB 3 WYDPLTKLWL 12

RESULT 80

ABJ00772 standard; peptide; 14 AA.

XX ABJ00772;

DT 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #46.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antiheumatic; anarthritic;
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;
 KW antiasthmatic; antiallergic; thyromimetic; antinaemic; haemostatic;
 KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 OS Unidentified.
 PN WO200216411-A2.
 PD 28-FEB-2002.
 XX 17-AUG-2001; 2001WO-US025850.
 PF 18-AUG-2000; 2000US-0226700P.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA Beltzner JP, Potter DM, Fleming TL, Rosen CA;
 PI WPI; 2002-499775/53.
 DR The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide.
 XX Claim 70; Page 215; 387pp; English.
 PS The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of BlyS binding polypeptide.
 CC The BlyS binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 64; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00094;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 1 WYDPLTKLML 10
 DB 3 WYDPLTKLML 12
 RESULT 81
 ID ABJ00774
 AC ABJ00774;
 XX 05-SEP-2002 (first entry)
 DT B lymphocyte affinity maturation library peptide #48.
 DB B lymphocyte stimulator protein binding protein; BlyS; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antiheumatic; antiarthritic;
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;

XX	antiaesthetic; anti-allergic; thyromimetic; antianemic; haemostatic;
KW	dermatological; anti-inflammatory; cardiac; ophthalmological; uropathic;
XX	antidiabetic; antithyroid; antidepressant; hepatotropic.
OS	Unidentified.
XX	
PN	WO200216411-A2.
XX	
PD	28-FEB-2002.
XX	
PF	17-AUG-2001; 2001WO-US025850.
XX	
PR	18-AUG-2000; 2000US-0226700P.
XX	
PA	(HDMA-) HUMAN GENOME SCI INC.
XX	
PI	Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX	
DR	WPI; 2002-499775/53.
XX	
PT	The treatment of various diseases e.g. rheumatoid arthritis, comprises
PR	administering B lymphocyte stimulator binding polypeptide.
XX	
PS	Claim 70; Page 215; 387pp; English.
XX	
CC	The present invention relates to the treatment, prevention or
CC	amelioration of a disease or disorder associated with: aberrant B
CC	lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells
CC	of haematopoietic origin; or proliferative disease; and reducing,
CC	inhibiting or stimulating immunoglobulin production, B cell proliferation
CC	and graft rejection involving administration of BLyS binding polypeptide.
CC	The BLyS binding polypeptides are used in the treatment, prevention or
CC	amelioration of diseases such as immune system diseases, proliferative
CC	diseases, diseases of cells of haematopoietic origin, graft rejection,
CC	allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC	hyperimmunoglobulinaemia, blood clotting disorders, ischaemia, and
CC	neurodegenerative diseases. The present sequence is a B lymphocyte
CC	stimulator protein binding peptide
XX	
SO	Sequence 14 AA;
XX	
QY	Query Match 100.0%; Score 64; DB 5; Length 14;
XX	Best Local Similarity 100.0%; Pred. No. 0.00094;
DB	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	
1	WYDPLTKLWL 10
3	WYDPLTKLWL 12
XX	
ID	ABJ00782 standard; peptide; 14 AA.
XX	
AC	ABJ00782;
XX	
DT	05-SEP-2002 (first entry)
XX	
DE	B lymphocyte affinity maturation library peptide #56.
XX	
KW	B lymphocyte stimulator protein binding protein; BLyS; immune disease;
KW	allergy; proliferative disease; infectious disease; arteriosclerosis;
KW	inflammatory disorder; hyperimmunoglobulinaemia; blood clotting;
KW	ischaemia; graft-versus-host disease; neurodegenerative disease;
KW	immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW	neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW	antiaesthetic; anti-allergic; thyromimetic; antianemic; haemostatic;
KW	dermatological; anti-inflammatory; cardiac; ophthalmological; uropathic;
XX	antidiabetic; antithyroid; antidepressant; hepatotropic.
OS	Unidentified.
XX	
PN	WO200216411-A2.

XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025850.
XX
XX 18-AUG-2000; 2000US-0226700P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;
XX WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 215; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
XX amelioration of a disease or disorder associated with: aberrant B
XX lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells
XX of haematopoietic origin; or proliferative disease; and reducing,
XX inhibiting or stimulating immunoglobulin production, B cell proliferation
XX and graft rejection involving administration of BLyS binding polypeptide.
XX The BLyS binding polypeptides are used in the treatment, prevention or
XX amelioration of diseases such as immune system diseases, proliferative
XX diseases, infectious diseases, arteriosclerosis, inflammatory disorders,
XX allergies, infectious diseases, blood clotting disorders, ischaemia, and
XX neurodegenerative diseases. The present sequence is a B lymphocyte
XX stimulator protein binding peptide
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12
RESULT 83
ABJ00787 standard; peptide; 14 AA.
XX
XX ABJ00787;
XX
XX 05-SEP-2002 (first entry)
XX
XX B lymphocyte affinity maturation library peptide #61.
XX
XX B lymphocyte stimulator protein binding protein; BLyS; immune disease;
XX allergy; proliferative disease; infectious disease; arteriosclerosis;
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX ischaemia; graft-versus-host disease; neurodegenerative disease;
XX immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
XX neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
XX antiasmatic; antiallergic; thymostimulant; antianemic; haemostatic;
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
XX antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX Unidentified.
OS
XX WO200216411-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025850.
XX
XX 18-AUG-2000; 2000US-0226700P.
XX
XX

PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;
XX WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 215; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
XX amelioration of a disease or disorder associated with: aberrant B
XX lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells
XX of haematopoietic origin; or proliferative disease; and reducing,
XX inhibiting or stimulating immunoglobulin production, B cell proliferation
XX and graft rejection involving administration of BLyS binding polypeptide.
XX The BLyS binding polypeptides are used in the treatment, prevention or
XX amelioration of diseases such as immune system diseases, proliferative
XX diseases, infectious diseases, arteriosclerosis, inflammatory disorders,
XX allergies, infectious diseases, blood clotting disorders, ischaemia, and
XX neurodegenerative diseases. The present sequence is a B lymphocyte
XX stimulator protein binding peptide
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12
RESULT 84
ABJ00788 standard; peptide; 14 AA.
XX
XX ABJ00788;
XX
XX 05-SEP-2002 (first entry)
XX
XX B lymphocyte affinity maturation library peptide #62.
XX
XX B lymphocyte stimulator protein binding protein; BLyS; immune disease;
XX allergy; proliferative disease; infectious disease; arteriosclerosis;
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX ischaemia; graft-versus-host disease; neurodegenerative disease;
XX immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
XX neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
XX antiasmatic; antiallergic; thymostimulant; antianemic; haemostatic;
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
XX antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX Unidentified.
OS
XX WO200216411-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025850.
XX
XX 18-AUG-2000; 2000US-0226700P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;
XX WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises

PT administering B lymphocyte stimulator binding polypeptide.
XX
PS Claim 70; Page 215; 387pp; English.
CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
|||||||
3 WYDPLTKLML 12
DB

RESULT 85
ABJ00807
ID ABJ00807 standard; peptide; 14 AA.
AC ABJ00807;
XX
DT 05-SEP-2002 (first entry)
XX
DE B lymphocyte affinity maturation library peptide #81.
XX
KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neutroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
PN WO200216411-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
DR WPI; 2002-499775/53.
XX
PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX
PS Claim 70; Page 215; 387pp; English.
XX
CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells

CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
|||||||
3 WYDPLTKLML 12
DB

RESULT 86
ABJ00819
ID ABJ00819 standard; peptide; 14 AA.
AC ABJ00819;
XX
DT 05-SEP-2002 (first entry)
XX
DE B lymphocyte affinity maturation library peptide #93.
XX
KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neutroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
PN WO200216411-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025850.
XX
PR 18-AUG-2000; 2000US-0226700P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
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DR WPI; 2002-499775/53.
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PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX
PS Claim 70; Page 215; 387pp; English.
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CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,

CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
DB 3 WYDPLTKLWL 12

RESULT 87
AB000838
ID AB000838 standard; peptide; 14 AA.

XX AC AB000838;

XX DT 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #112.

KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX OS Unidentified.

XX PN WO200216411-A2.

XX PD 28-FEB-2002.

XX PF 17-AUG-2001; 2001WO-US025850.

XX PR 18-AUG-2000; 2000US-0226700P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Belzer JP, Potter DM, Fleming TL, Rosen CA;

XX PS WPI; 2002-499775/53.

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 216; 387pp; English.

CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
DB 3 WYDPLTKLWL 12

RESULT 88
AB000751
ID AB000751 standard; peptide; 14 AA.

XX AC AB000751;

XX DT 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #25.

KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX OS Unidentified.

XX PN WO200216411-A2.

XX PD 28-FEB-2002.

XX PF 17-AUG-2001; 2001WO-US025850.

XX PR 18-AUG-2000; 2000US-0226700P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Belzer JP, Potter DM, Fleming TL, Rosen CA;

XX PS WPI; 2002-499775/53.

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 214; 387pp; English.

CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
DB 3 WYDPLTKLWL 12

XX	ABJ00767	standard; peptide; 14 AA.
XX	ABJ00767;	
XX	05-SEP-2002	(first entry)
DE		B lymphocyte affinity maturation library peptide #41.
XX		
XX		B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW		allergy; proliferative disease; infectious disease; arteriosclerosis;
KW		inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW		ischaemia; graft-versus-host disease; neurodegenerative disease;
KW		immunosuppressive; nephrotropic; antirheumatic; anarthritic;
KW		neuroprotective; cystostatic; immunostimulant; antitumor; anti-HIV;
KW		antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;
KW		dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
KW		antidiabetic; antithyroid; antidepressant; hepatotropic.
XX		
OS		Unidentified.
PN		WO200216411-A2.
XX		
PD		28-FEB-2002.
XX		
PF		17-AUG-2001; 2001WO-US025850.
XX		
PR		18-AUG-2000; 2000US-0226700P.
XX		
PA		(HUMA-) HUMAN GENOME SCI INC.
PI		Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX		
DR		WPI; 2002-499775/53.
XX		
PT		The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT		administering B lymphocyte stimulator binding polypeptide.
XX		
PS		Claim 70; Page 214; 387pp; English.
XX		
CC		The present invention relates to the treatment, prevention or
CC		amelioration of a disease or disorder associated with: aberrant B
CC		lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC		of haematopoietic origin; or proliferative disease; and reducing,
CC		inhibiting or stimulating immunoglobulin production, B cell proliferation
CC		and graft rejection involving administration of BlyS binding polypeptide.
CC		The BlyS binding polypeptides are used in the treatment, prevention or
CC		amelioration of diseases such as immune system diseases, proliferative
CC		diseases, diseases of cells of hematopoietic origin, graft rejection,
CC		allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC		hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC		neurodegenerative diseases. The present sequence is a B lymphocyte
CC		stimulator protein binding peptide
XX		
SQ		Sequence 14 AA;
	Query Match	100.0%; Score 64; DB 5; Length 14;
	Best Local Similarity	100.0%; Pred. No. 0.00094;
	Matches 10; Conservative	0; Mismatches 0; Indels 0; Gaps 0.0;
OY		
	1 WYDPLTKLWL 10	
	3 WYDPLTKLWL 12	
DB		
	RESULT 90	
	ABJ00784	
ID	ABJ00784	standard; peptide; 14 AA.
XX	ABJ00784;	
XX		

DT	05-SEP-2002	(first entry)
DE	B lymphocyte affinity maturation library peptide #58.	
KM	B lymphocyte stimulator protein binding protein; BlyS; immune disease;	
KM	allergy; proliferative disease; infectious disease; arteriosclerosis;	
KM	inflammatory disorder; hypergammaglobulinaemia; blood clotting;	
KM	ischaemia; graft-versus-host disease; neurodegenerative disease;	
KM	immunosuppressive; nephrotropic; antirheumatic; antiarthritic;	
KM	neuroprotective; cytosolic; immunostimulant; antitumour; anti-HIV;	
KM	antiasmatic; anti-allergic; thyromimetic; antinausea; haemostatic;	
KM	dermatological; anti-inflammatory; cardiac; ophthalmological; uropathic;	
XX	antidiabetic; antithyroid; antidepressant; hepatotropic.	
OS	Unidentified.	
XX		
PN	WO200216411-A2.	
PD		
XX	28-FEB-2002.	
PF	17-AUG-2001; 2001WO-US025850.	
XX		
PR	18-AUG-2000; 2000US-0226700P.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
PI	Beltzer JP, Potter DM, Fleming TL, Rosen CA;	
XX		
DR	WPI, 2002-499775/53.	
XX		
PT	The treatment of various diseases e.g. Rheumatoid arthritis, comprises	
PT	administering B lymphocyte stimulator binding polypeptide.	
XX		
PS	Claim 70; Page 215; 387pp; English.	
XX		
CC	The present invention relates to the treatment, prevention or	
CC	amelioration of a disease or disorder associated with aberrant B	
CC	lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells	
CC	of haematopoietic origin; or proliferative disease; and reducing,	
CC	inhibiting or stimulating immunoglobulin production, B cell proliferation	
CC	and graft rejection involving administration of BlyS binding polypeptide.	
CC	The BlyS binding polypeptides are used in the treatment, prevention or	
CC	amelioration of diseases such as immune system diseases, proliferative	
CC	diseases, diseases of cells of hematopoietic origin, graft rejection,	
CC	allergies, infectious diseases, arteriosclerosis, inflammatory disorders,	
CC	hypergammaglobulinaemia, blood clotting disorders, ischaemia, and	
CC	neurodegenerative diseases. The present sequence is a B lymphocyte	
XX	stimulator protein binding peptide	
XX		
SO	Sequence 14 AA;	
XX		
Query Match	100.0%;	Score 64; DB 5; Length 14;
Best Local Similarity	100.0%;	Pred. NO. 0.0009%;
Matches 10; Conservative 0;	Mismatches 0;	Indels 0; Gaps 0.
Qy	1 WYDPLTKLML 10	
Db	3 WYDPLTKLML 12	
RESULT 91		
ID	ABJ00795	
XX	ABJ00795 standard; peptide; 14 AA.	
AC	ABJ00795;	
XX		
DT	05-SEP-2002 (first entry)	
XX		
DE	B lymphocyte affinity maturation library peptide #69.	
KM	B lymphocyte stimulator protein binding protein; BlyS; immune disease;	
KM	allergy; proliferative disease; infectious disease; arteriosclerosis;	
KM	inflammatory disorder; hypergammaglobulinaemia; blood clotting;	

ischaemia; graft-versus-host disease; neurodegenerative disease;
immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
XX WO200216411-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025850.
XX
XX 18-AUG-2000; 2000US-0226700P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
XX WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 215; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
XX amelioration of a disease or disorder associated with: aberrant B
XX lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
XX of haematopoietic origin; or proliferative disease; and reducing,
XX inhibiting or stimulating immunoglobulin production, B cell proliferation
XX and graft rejection involving administration of BlyS binding polypeptide.
XX The BlyS binding polypeptides are used in the treatment, prevention or
XX amelioration of diseases such as immune system diseases, proliferative
XX diseases, diseases of cells of hematopoietic origin, graft rejection,
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX neurodegenerative diseases. The present sequence is a B lymphocyte
XX stimulator protein binding peptide
XX
SQ Sequence 14 AA;
XX
XX Query Match 100.0%; Score 64; DB 5; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 0.00094;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 WYDPLTKLWL 10
XX |||||||
XX 3 WYDPLTKLWL 12
XX
Db 3 WYDPLTKLWL 12
XX
RESULT 92
XX ABJ00804 standard; peptide; 14 AA.
XX
XX ABJ00804;
XX
XX 05-SEP-2002 (first entry)
XX
XX B lymphocyte affinity maturation library peptide #78.
XX
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
XX allergy; proliferative disease; infectious disease; arteriosclerosis;
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX ischaemia; graft-versus-host disease; neurodegenerative disease;
XX immunosuppressive; nephrotropic; antirheumatic; antitumour;
XX neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
XX antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
XX antidiabetic; antithyroid; antidepressant; hepatotropic.
XX

OS Unidentified.
XX
XX WO200216411-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025850.
XX
XX 18-AUG-2000; 2000US-0226700P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
XX WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 215; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
XX amelioration of a disease or disorder associated with: aberrant B
XX lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
XX of haematopoietic origin; or proliferative disease; and reducing,
XX inhibiting or stimulating immunoglobulin production, B cell proliferation
XX and graft rejection involving administration of BlyS binding polypeptide.
XX The BlyS binding polypeptides are used in the treatment, prevention or
XX amelioration of diseases such as immune system diseases, proliferative
XX diseases, diseases of cells of hematopoietic origin, graft rejection,
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX neurodegenerative diseases. The present sequence is a B lymphocyte
XX stimulator protein binding peptide
XX
SQ Sequence 14 AA;
XX
XX Query Match 100.0%; Score 64; DB 5; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 0.00094;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 WYDPLTKLWL 10
XX |||||||
XX 3 WYDPLTKLWL 12
XX
Db 3 WYDPLTKLWL 12
XX
RESULT 93
XX ABJ00820 standard; peptide; 14 AA.
XX
XX ABJ00820;
XX
XX 05-SEP-2002 (first entry)
XX
XX B lymphocyte affinity maturation library peptide #94.
XX
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
XX allergy; proliferative disease; infectious disease; arteriosclerosis;
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX ischaemia; graft-versus-host disease; neurodegenerative disease;
XX immunosuppressive; nephrotropic; antirheumatic; antitumour;
XX neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
XX antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
XX antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX Unidentified.
XX
XX WO200216411-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025850.
XX

XX 18-AUG-2000; 2000US-0226700P.
PR (HUMA-) HUMAN GENOME SCT INC.
XX
XX Beltzer JP, Porter DM, Fleming TL, Rosen CA;
PI WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 216; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving immunoglobulin production of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLML 10
|||
3 WYDPLTKLML 12
Db
RESULT 94
ABJ00828
ID ABJ00828 standard; peptide; 14 AA.
XX
XX ABJ00828;
AC
XX
XX 05-SEP-2002 (first entry)
DT
XX
XX B lymphocyte affinity maturation library peptide #102.
DE
XX
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthmetic; anti-allergic; thymomimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX Unidentified.
OS
XX
XX WO200216411-A2.
PN
XX
XX 28-FEB-2002.
PD
XX
XX 17-AUG-2001; 2001WO-US025850.
PF
XX
XX 18-AUG-2000; 2000US-0226700P.
PR
XX
XX (HUMA-) HUMAN GENOME SCT INC.
PA
XX
XX Beltzer JP, Porter DM, Fleming TL, Rosen CA;
PI

DR WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 216; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving immunoglobulin production of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLML 10
|||
3 WYDPLTKLML 12
Db
RESULT 95
ABJ00734
ID ABJ00734 standard; peptide; 14 AA.
XX
XX ABJ00734;
AC
XX
XX 05-SEP-2002 (first entry)
DT
XX
XX B lymphocyte affinity maturation library peptide #8.
DE
XX
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthmetic; anti-allergic; thymomimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX Unidentified.
OS
XX
XX WO200216411-A2.
PN
XX
XX 28-FEB-2002.
PD
XX
XX 17-AUG-2001; 2001WO-US025850.
PF
XX
XX 18-AUG-2000; 2000US-0226700P.
PR
XX
XX (HUMA-) HUMAN GENOME SCT INC.
PA
XX
XX Beltzer JP, Porter DM, Fleming TL, Rosen CA;
PI WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 70; Page 214; 387pp; English.
XX

CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing, preventing
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match	100.0%	Score 64	DB 5	Length 14
Best Local Similarity	100.0%	Pred No.	0.00094	
Matches 10	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	1	WYDPLTKLWL	10
Db	3	WYDPLTKLWL	12

RESULT 96
ABJ00743
ID ABJ00743 standard; peptide; 14 AA

AC ABJ00743;
XX
DT 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #17.

KW B lymphocyte stimulator protein binding protein; BvS; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hyperimmunoglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antihumanetic; antiarthritis;
 KW neuroprotective; cytosolic; immunostimulant; antitumour; anti-HIV;
 KW antiaesthetic; antiallergic; thymostimulant; antianemic; haemostatic;
 KW dermatological; antinflammatory; cardiac; ophthalmological; uropathic;
 KW antidiabetic; antihypertoid; antidepressant; hepatotropic.

OS Unidentified.

PN WO200216411-A2

PD 28-FEB-2002.

PF 17-AUG-2001; 2001WO-US025850

PR 18-AUG-2000; 2000US-0226700P.

PA (HUMA-) HUMAN GENOME SCI INC
PA
PA

PI Beltzer JP, Potter DM, Fleming TL, Rosen CA, ...

DR WPI; 2002-499775/53.

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises administering B Lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 214; 387pp; English.

CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blyts), Blyts receptor expression or activity; cells
CC of hematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blyts binding polypeptide.
CC The Blyts binding polypeptides are used in the treatment, prevention or

CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disor-
CC hypermagnoglobulinemia, blood clotting disorders, ischemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide

Query Match	100.0%	Score 64	DB 5	Length 14
Best Local Similarity	100.0%	Pred. NO.	0.0009%	
Matches 10	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 1 WYDPLTKLWL 10
|||
Db 3 WYDPLTKLWL 12

RESULT 97
ABJ00745
ID ABJ00745 standard; peptide; 14 AA

AC	ABJ00745;
XX	
DT	05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #19.

KM B-lymphocyte stimulator; protein binding protein; BLVS; immune disease;
KM allergy; proliferative disease; infectious disease; arexiosclerosis;
KM inflammatory disorder; hypermagglotulinemia; blood clotting;
KM ischaemia, graft-versus-host disease; neurodegenerative disease;
KM immunosuppressive, nephrotropic, antineumatic, antiarthritic;
KM neuroprotective; cytosolatic; immunostimulant; antitumour; anti-HIV;
KM antiaesthetic; antiallergic; thyromimetic; antitenseic; haemostatic;
KM dermatological; antinflammatory; cardiant; ophthalmological; uropathic;
KM antidiabetic; antihypoid; antidepressant; hepatotropic.

OS Unidentified.

PN WO200216411-A2.

PD 28-FEB-2002

PF 17-AUG-2001; 2001WO-US025850.

PR 18-AUG-2000; 2000US-0226700P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Beltzer JP, Potter DM, Fleming TL, Rosen CA,

DR WPI; 2002-499775/53.

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 214; 387pp; English

CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing
CC inhibiting or stimulating immunoglobulin production, B cell proliferation,
CC and graft rejection involving administration of BLyS binding polypeptide.
CC The BLyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, atrexioclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide

SO Sequence 14 AA; Score 64; DB 5; Length 14;
Query Match Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WYDPLTKLML 10
3 WYDPLTKLML 12

Db 3 WYDPLTKLML 12

RESULT 98
ABJ00759
ID ABJ00759 standard; peptide; 14 AA.
AC ABJ00759;
DT 05-SEP-2002 (first entry)

XX B lymphocyte affinity maturation library peptide #33.
XX
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX
XX Unidentified.
OS
XX
XX WO200216411-A2.
PN
XX
XX 28-FEB-2002.
PD
XX
XX 17-AUG-2001; 2001WO-US025850.
PF
XX
XX 18-AUG-2000; 2000US-0226700P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
PI
XX
XX WPI; 2002-499775/53.
DR
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
PT
XX
XX Claim 70; Page 214; 387pp; English.
PS
XX
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
XX
XX Sequence 14 AA;

Query Match Best Local Similarity 100.0%; Score 64; DB 5; Length 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WYDPLTKLML 10
3 WYDPLTKLML 12

Db 1 WYDPLTKLML 10

Db 3 WYDPLTKLML 12

RESULT 99
ABJ00778
ID ABJ00778 standard; peptide; 14 AA.
AC ABJ00778;
DT 05-SEP-2002 (first entry)

XX B lymphocyte affinity maturation library peptide #52.
XX
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX
XX Unidentified.
OS
XX
XX WO200216411-A2.
PN
XX
XX 28-FEB-2002.
PD
XX
XX 17-AUG-2001; 2001WO-US025850.
PF
XX
XX 18-AUG-2000; 2000US-0226700P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
PI
XX
XX WPI; 2002-499775/53.
DR
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
PT
XX
XX Claim 70; Page 215; 387pp; English.
PS
XX
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
XX
XX Sequence 14 AA;

Query Match Best Local Similarity 100.0%; Score 64; DB 5; Length 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WYDPLTKLML 10
3 WYDPLTKLML 12

Db 3 WYDPLTKLML 12

RESULT 100
ABJ00796
ID ABJ00796 standard; peptide; 14 AA.

XX ABQ00796;
 XX
 AC
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE B lymphocyte affinity maturation library peptide #70.
 XX
 KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW neuromuscular; cytosolic; immunostimulant; antitumor; anti-HIV;
 KW antidiabetic; antiallergic; thymine; antianemic; haemostatic;
 KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX
 OS Unidentified.
 XX
 PN WO200216411-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-US025850.
 XX
 PR 18-AUG-2000; 2000US-0226700P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
 XX
 DR WPI; 2002-499775/53.
 XX
 PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
 XX administering B lymphocyte stimulator binding polypeptide.
 PS Claim 70; Page 215; 387pp; English.
 XX
 CC The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of Blys binding polypeptide.
 CC The Blys binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of haematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 XX
 SQ Sequence 14 AA;
 QY Query Match 100.0%; Score 64; DB 5; Length 14;
 DB Best Local Similarity 100.0%; Pred. No. 0.00094; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;
 1 WYDPLTKLWL 10
 3 WYDPLTKLWL 12

Search completed: July 12, 2004, 21:28:48
 Job time : 55 secs

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OM protein - protein search, using sw model

Run on: July 12, 2004, 21:23:57 ; Search time 21 Seconds
(without alignments)
22.446 Million cell updates/sec

Title: US-09-932-613-457
Perfect score: 64
Sequence: 1 WYDPLTKML 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
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2	42	65.6	49	4	US-09-636-791A-18
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5	42	65.6	642	4	US-09-337-307A-4
6	41	64.1	593	4	US-09-328-352-4866
7	41	64.1	685	4	US-09-252-991A-31711
8	39	60.9	193	4	US-09-489-039A-12391
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14	39	60.9	941	3	US-09-179-558-55
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16	39	60.9	941	4	US-09-722-487-55
17	39	60.9	941	4	US-09-722-708-55
18	38	59.4	345	4	US-09-252-991A-21042
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22	37.5	58.6	301	3	US-08-852-730-20
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25	37	57.8	158	4	US-09-834-759-508
26	37	57.8	243	4	US-09-834-759-507
27	37	57.8	311	4	US-09-489-039A-8990

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37	36	56.2	321	4	US-09-688-019-2	Sequence 2, Appli
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129	35	54.7	1153	3	US-08-665-574C-14	Sequence 14, Appl1	202	33	51.6	340	4	US-09-312-283C-143	Sequence 143, App
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289 32 50.0 530 3 US-09-252-586-2 Sequence 2, Appl
290 32 50.0 531 3 US-08-688-988-38 Sequence 38, Appl
291 32 50.0 532 3 US-09-181-336-15 Sequence 15, Appl
292 32 50.0 543 2 US-08-922-170B-10 Sequence 10, Appl
293 32 50.0 543 3 US-09-071-739B-2 Sequence 2, Appl
294 32 50.0 543 3 US-09-181-336-13 Sequence 13, Appl
295 32 50.0 543 4 US-09-260-038B-2 Sequence 2, Appl
296 32 50.0 543 4 US-09-739-455-4 Sequence 4, Appl
297 32 50.0 543 4 US-09-739-455-14 Sequence 14, Appl
298 32 50.0 543 4 US-09-635-923-2 Sequence 2, Appl
299 32 50.0 543 4 US-09-487-716A-2 Sequence 2, Appl
300 32 50.0 543 4 US-09-322-977-2 Sequence 2, Appl
```

ALIGNMENTS

```
RESULT 1
US-09-621-976-7356
; Sequence 7356, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
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; SEQ ID NO 7356
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-7356
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Query Match
Best Local Similarity 68.8%; Score 44; DB 4; Length 52;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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```
QY
1 WYDPLTKLM 9
|||:|:|
26 WYTPNKKLM 34
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```
RESULT 2
US-09-636-791A-18
; Sequence 18, Application US/09636791A
; Patent No. 6503703
; GENERAL INFORMATION:
```

```
; APPLICANT: Palese et al
; TITLE OF INVENTION: IDENTIFICATION AND USE OF ANTIVIRAL COMPOUNDS THAT
; TITLE OF INVENTION: INHIBIT INTERACTION OF HOST CELL PROTEINS AND VIRAL
; FILE REFERENCE: 6923-077-999
; CURRENT APPLICATION NUMBER: US/09/636,791A
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,263
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
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SEQ ID NO 18
LENGTH: 49
TYPE: PRT
ORGANISM: Homo sapiens
US-09-636-791A-18
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Query Match
Best Local Similarity 65.6%; Score 42; DB 4; Length 49;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY
2 YDPLTKLM 9
||:||||
22 FDPVTKLM 29
```

```
RESULT 3
US-09-636-791A-15
; Sequence 15, Application US/09636791A
; Patent No. 6503703
; GENERAL INFORMATION:
```

```
; APPLICANT: Palese et al
; TITLE OF INVENTION: IDENTIFICATION AND USE OF ANTIVIRAL COMPOUNDS THAT
; TITLE OF INVENTION: INHIBIT INTERACTION OF HOST CELL PROTEINS AND VIRAL
; FILE REFERENCE: 6923-077-999
; CURRENT APPLICATION NUMBER: US/09/636,791A
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,263
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
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SEQ ID NO 15
LENGTH: 619
TYPE: PRT
ORGANISM: Homo sapiens
US-09-636-791A-15
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Query Match
Best Local Similarity 65.6%; Score 42; DB 4; Length 619;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY
2 YDPLTKLM 9
```

Db 485 FDPVTKLM 492

RESULT 4

US-09-337-307A-3

Sequence 3, Application US/09337307A

Patent No. 6432692

GENERAL INFORMATION:

APPLICANT: Bradfield, Christopher A.

APPLICANT: Carver, Lucy A.

APPLICANT: Dunham, Elizabeth E.

TITLE OF INVENTION: Sensitive Biosay For Detecting Agonists Of The Aryl Hydrocarbon

FILE REFERENCE: WARP0105

CURRENT APPLICATION NUMBER: US/09/337,307A

CURRENT FILING DATE: 1999-06-21

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 642

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: /note = "ARA3"

US-09-337-307A-3

Query Match

Best Local Similarity 65.6%; Score 42; DB 4; Length 642;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9

Db 485 FDPVTKLM 492

RESULT 5

US-09-337-307A-4

Sequence 4, Application US/09337307A

Patent No. 6432692

GENERAL INFORMATION:

APPLICANT: Bradfield, Christopher A.

APPLICANT: Carver, Lucy A.

APPLICANT: Dunham, Elizabeth E.

TITLE OF INVENTION: Sensitive Biosay For Detecting Agonists Of The Aryl Hydrocarbon

FILE REFERENCE: WARP0105

CURRENT APPLICATION NUMBER: US/09/337,307A

CURRENT FILING DATE: 1999-06-21

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 642

TYPE: PRT

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: /note = "ARA3"

US-09-337-307A-4

Query Match

Best Local Similarity 65.6%; Score 42; DB 4; Length 642;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9

Db 485 FDPVTKLM 492

RESULT 6

US-09-328-352-4866

Sequence 4866, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4866

LENGTH: 593

TYPE: PRT

ORGANISM: Acinetobacter baumannii

US-09-328-352-4866

Query Match

Best Local Similarity 64.1%; Score 41; DB 4; Length 593;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 10

Db 49 YDPLNITLM 57

RESULT 7

US-09-252-991A-31711

Sequence 31711, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31711

LENGTH: 685

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-31711

Query Match

Best Local Similarity 64.1%; Score 41; DB 4; Length 685;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 10

Db 579 WFDPSGRMT 588

RESULT 8

US-09-489-039A-12391

Sequence 12391, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 12391

LENGTH: 193

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-12391

Query Match 60.9%; Score 39; DB 4; Length 193;
Best Local Similarity 58.3%; Pred. No. 40;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 WYD--PLTKWL 10
Db 83 WYVSPPLKLMW 94

RESULT 9

US-09-489-039A-9029
; Sequence 9029, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9029
; LENGTH: 410
; TYPE: PRF
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9029

Query Match 60.9%; Score 39; DB 4; Length 410;
Best Local Similarity 50.0%; Pred. No. 85;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKWL 10
Db 241 WYDVNCIMWL 250

RESULT 10
US-09-179-558-56
; Sequence 56, Application US/09179558
; Patent No. 6180612
; GENERAL INFORMATION:
; APPLICANT: Hockensmith, Joel W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TARGETING DNA METABOLIC PROCESSES USING
; TITLE OF INVENTION: AMINOGLYCOSIDE DERIVATIVES
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/179,558
; FILING DATE: 27-OCT-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: U.S. 09/060,470
; FILING DATE: 15-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 60/063,898
; FILING DATE: 31-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 9426-005-999
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)7909090
; TELEFAX: (212)8699741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:
; LENGTH: 727 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-179-558-56

Query Match 60.9%; Score 39; DB 3; Length 727;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKW 9
Db 53 YDPAKTKW 60

RESULT 11
US-09-722-825-56
; Sequence 56, Application US/09722825
; Patent No. 6531306
; GENERAL INFORMATION:
; APPLICANT: Hockensmith, Joel W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TARGETING DNA METABOLIC PROCESSES USING
; TITLE OF INVENTION: AMINOGLYCOSIDE DERIVATIVES
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/722,825
; FILING DATE: 28-Nov. 6531306-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/179,558
; FILING DATE: <Unknown>
; APPLICATION NUMBER: U.S. 60/063,898
; FILING DATE: 31-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 9426-005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)7909090
; TELEFAX: (212)8699741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-722-825-56

Query Match 60.9%; Score 39; DB 4; Length 727;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLM 9
Db 53 YDPATKTM 60

RESULT 12
US-09-722-487-56
Sequence 56, Application US/09722487
Patent No. 6537791
GENERAL INFORMATION:
APPLICANT: Hockensmith, Joel W.
Muthuswami, Rohini
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TARGETING DNA METABOLIC PROCESSES USING
AMINOGLYCOSIDE DERIVATIVES
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/722,487
FILING DATE: 28-No. 6537791-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/179,558
FILING DATE: <Unknown>
APPLICATION NUMBER: U.S. 60/063,898
FILING DATE: 31-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 9426-005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 727 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-722-487-56

Query Match 60.9%; Score 39; DB 4; Length 727;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLM 9
Db 53 YDPATKTM 60

RESULT 13
US-09-722-708-56
Sequence 56, Application US/09722708
Patent No. 6573060

GENERAL INFORMATION:
APPLICANT: Hockensmith, Joel W.
Muthuswami, Rohini
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TARGETING DNA METABOLIC PROCESSES USING
AMINOGLYCOSIDE DERIVATIVES
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/722,708
FILING DATE: 28-No. 6573060-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/179,558
FILING DATE: <Unknown>
APPLICATION NUMBER: U.S. 60/063,898
FILING DATE: 31-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 9426-005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 727 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-722-708-56

Query Match 60.9%; Score 39; DB 4; Length 727;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLM 9
Db 53 YDPATKTM 60

RESULT 14
US-09-179-558-55
Sequence 55, Application US/09179558
Patent No. 6180612
GENERAL INFORMATION:
APPLICANT: Hockensmith, Joel W.
Muthuswami, Rohini
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TARGETING DNA METABOLIC PROCESSES USING
AMINOGLYCOSIDE DERIVATIVES
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/179,558
FILING DATE: 27-OCT-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 09/060,470
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 60/063,898
FILING DATE: 31-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 9426-005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-179-558-55

Query Match 60.9%; Score 39; DB 3; Length 941;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLM 9
Db 267 YDPATKTM 274

RESULT 15
US-09-722-825-55
Sequence 55, Application US/09722825
Patent No. 6531306
GENERAL INFORMATION:
APPLICANT: Hockensmith, Joel W.
Muthuswami, Rohini
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TARGETING DNA METABOLIC PROCESSES USING
AMINOGLYCOSIDE DERIVATIVES
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/722,825
FILING DATE: 28-No. 6531306-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/179,558
FILING DATE: <Unknown>
APPLICATION NUMBER: U.S. 60/063,898
FILING DATE: 31-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 9426-005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-722-825-55

Query Match 60.9%; Score 39; DB 4; Length 941;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLM 9
Db 267 YDPATKTM 274

RESULT 16
US-09-722-487-55
Sequence 55, Application US/09722487
Patent No. 6537791
GENERAL INFORMATION:
APPLICANT: Hockensmith, Joel W.
Muthuswami, Rohini
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TARGETING DNA METABOLIC PROCESSES USING
AMINOGLYCOSIDE DERIVATIVES
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/722,487
FILING DATE: 28-No. 6537791-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/179,558
FILING DATE: <Unknown>
APPLICATION NUMBER: U.S. 60/063,898
FILING DATE: 31-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 9426-005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-722-487-55

Query Match 60.9%; Score 39; DB 4; Length 941;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKM 9
Db 267 YDPATKM 274

RESULT 17
US-09-722-708-55
Sequence 55, Application US/09722708
Patent No. 6573060
GENERAL INFORMATION:
APPLICANT: Hockensmith, Joel W.
Muthuswami, Rohini

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TARGETING DNA METABOLIC PROCESSES USING
AMINOGLYCOSIDE DERIVATIVES

NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/722,708
FILING DATE: 28-No. 6573060-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/179,558
FILING DATE: <Unknown>
APPLICATION NUMBER: U.S. 60/063,898
FILING DATE: 31-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 9426-005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-722-708-55

Query Match 60.9%; Score 39; DB 4; Length 941;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKM 9
Db 267 YDPATKM 274

RESULT 18

US-09-252-991A-21042
Sequence 21042, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21042
LENGTH: 345
TYPE: PRT

ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21042

Query Match 59.4%; Score 38; DB 4; Length 345;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DPLTKM 9
Db 188 DPLTKM 194

RESULT 19
US-09-328-352-8180
Sequence 8180, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-039A
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8180
LENGTH: 780
TYPE: PRT

ORGANISM: Acinetobacter baumannii
US-09-328-352-8180

Query Match 59.4%; Score 38; DB 4; Length 780;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKML 10
Db 647 WYDPRGVLM 656

RESULT 20
US-08-674-168-31
Sequence 31, Application US/08674168
Patent No. 5804414
GENERAL INFORMATION:
APPLICANT: MORIYA, Mika
APPLICANT: MATSUI, Hiroshi
APPLICANT: YOKOZAKI, Kenzo
APPLICANT: HIRANO, Seiko
APPLICANT: HAYAKAWA, Akiyoshi
APPLICANT: IZUI, Masako
APPLICANT: SUGIMOTO, Masakazu
TITLE OF INVENTION: METHOD OF AMPLIFYING GENE USING
TITLE OF INVENTION: ARTIFICIAL TRANSPOSON
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/674,168
FILING DATE: 01-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-166541
FILING DATE: 30-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-810-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 24865 OPAT UR
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-674-168-31

Query Match 58.6%; Score 37.5; DB 1; Length 301;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 1 WY--DPLTKLWL 10
Db 193 WYSGDDPLNLVWL 205

RESULT 21
US-08-985-908-15
Sequence 15, Application US/08985908
Patent No. 6004773
GENERAL INFORMATION:
APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI NA
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,908
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325659
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON

REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-908-15

Query Match 58.6%; Score 37.5; DB 3; Length 301;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 1 WY--DPLTKLWL 10
Db 193 WYSGDDPLNLVWL 205

RESULT 22
US-08-852-730-20
Sequence 20, Application US/08852730
Patent No. 6090597
GENERAL INFORMATION:
APPLICANT: SEIRO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,
APPLICANT: MASAKO IZU, ATSUSHI HAYAKAWA, YASUHIKO YOSHIHARA, AND TSUYOSHI
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
ZIP: 22026
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,730
FILING DATE: 05-07-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-142812
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-730-20

Query Match 58.6%; Score 37.5; DB 3; Length 301;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 1 WY--DPLTKLWL 10
Db 193 WYSGDDPLNLVWL 205

RESULT 23

```
US-09-328-352-8223
; Sequence 8223, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 8223
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8223

Query Match          57.8%; Score 37; DB 4; Length 79;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
   |||||
   :
Db 38 WLSPLTKMKI 47

RESULT 24
US-09-621-976-6153
; Sequence 6153, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6153
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6153

Query Match          57.8%; Score 37; DB 4; Length 93;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 1 WYD---PLTKML 10
   |||||
   :
Db 42 WIDISVPLTSLMI 55

RESULT 25
US-09-834-759-508
; Sequence 508, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
```

```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 508
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-508

Query Match          57.8%; Score 37; DB 4; Length 158;
Best Local Similarity 62.5%; Pred. No. 69;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9
   |||||
   :
Db 27 YNPLTNIM 34

RESULT 26
US-09-834-759-507
; Sequence 507, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 507
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-507

Query Match          57.8%; Score 37; DB 4; Length 243;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9
   |||||
   :
Db 27 YNPLTNIM 34

RESULT 27
US-09-489-039A-8990
; Sequence 8990, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8990
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8990

Query Match          57.8%; Score 37; DB 4; Length 311;
Best Local Similarity 58.3%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
```

Qy 1 WY--DPLTKLWL 10
|||
Db 96 WYRNDPRASLWL 107

RESULT 28

US-09-041-718-3
; Sequence 3, Application US/09041718A
; Patent No. 6225075
; GENERAL INFORMATION:
; APPLICANT: Bard, Martin
; TITLE OF INVENTION: DNA encoding sterol methyltransferase
; FILE REFERENCE: 740,003US1
; CURRENT APPLICATION NUMBER: US/09/041,718A
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-041-718-3

Query Match 57.8%; Score 37; DB 3; Length 383;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 9
|||
Db 286 WYYPPLTGEM 294

RESULT 29

US-09-328-352-5102
; Sequence 5102, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5102
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5102

Query Match 57.8%; Score 37; DB 4; Length 437;
Best Local Similarity 44.4%; Pred. No. 1.9e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 9
|||
Db 15 WYDPLRSSW 23

RESULT 30

US-09-976-594-369
; Sequence 369, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 369
; LENGTH: 819
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Inocyte ID No. 6673549 2125081CD1
US-09-976-594-369

Query Match 57.8%; Score 37; DB 4; Length 819;
Best Local Similarity 60.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10
|||
Db 626 WYBPLOKFL 635

RESULT 31

US-08-680-326-41
; Sequence 41, Application US/08680326
; Patent No. 5925733
; GENERAL INFORMATION:
; APPLICANT: ROSE, TIMOTHY M.
; APPLICANT: BOSCH, MARINX
; APPLICANT: STRAND, KURT
; APPLICANT: TODARO, GEORGE J.
; TITLE OF INVENTION: DNA POLYMERASE OF GAMMA HERPES VIRUSES
; TITLE OF INVENTION: ASSOCIATED WITH KAPOSI'S SARCOMA AND RETROPERITONEAL
; NUMBER OF SEQUENCES: 152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680,326
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 29938-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 985 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-680-326-41

Query Match 57.8%; Score 37; DB 2; Length 985;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

Qy 1 WY--DPLTKLWL 10
|||
Db 893 WYVVDPLTGIMW 904

```
RESULT 32
US-08-164-292B-18
; Sequence 18, Application US/08164292B
; Patent No. 5820868
; GENERAL INFORMATION:
; APPLICANT: MITTAL, SURESH K.
; APPLICANT: GRAHAM, FRANK L.
; APPLICANT: PREVEC, LUDVIG
; APPLICANT: BABIUK, LORNE A.
; TITLE OF INVENTION: RECOMBINANT PROTEIN PRODUCTION IN BOVINE
; TITLE OF INVENTION: ADENOVIRUS EXPRESSION VECTOR SYSTEM
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 345 California Street
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104-2675
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,292B
; FILING DATE: 09-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 29310-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 677-7000
; TELEFAX: (415) 677-7522
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-164-292B-18

Query Match          56.2%; Score 36; DB 2; Length 308;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
; ORGANISM: Bovine adenovirus type 3
US-08-845-623-18
Query Match          56.2%; Score 36; DB 3; Length 308;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 YDPLTKLML 10
DB      71 YNPFTVLM 79

RESULT 34
US-08-815-927-18
; Sequence 18, Application US/08815927
; Patent No. 6086890
; GENERAL INFORMATION:
; APPLICANT: MITTAL, SURESH K.
; APPLICANT: GRAHAM, FRANK L.
; APPLICANT: PREVEC, LUDVIG
; APPLICANT: BABIUK, LORNE A.
; TITLE OF INVENTION: RECOMBINANT PROTEIN PRODUCTION IN BOVINE ADENOVIRUS EXPRESSION
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 293102002101
; CURRENT APPLICATION NUMBER: US/08/815,927
; CURRENT FILING DATE: 1997-03-13
; EARLIER APPLICATION NUMBER: 08/164,294
; EARLIER FILING DATE: 1993-12-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Bovine adenovirus type 3
; US-08-815-927-18

Query Match          56.2%; Score 36; DB 3; Length 308;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 YDPLTKLML 10
DB      71 YNPFTVLM 79

RESULT 35
US-09-103-330-18
; Sequence 18, Application US/09103330A
; Patent No. 6319716
; GENERAL INFORMATION:
; APPLICANT: TIKOO, SURESH K.
; APPLICANT: BABIUK, LORNE A.
; APPLICANT: REDDY, POLICE S.
; TITLE OF INVENTION: ISOLATION OF MUTANTS IN THE E3 REGION OF THE
; TITLE OF INVENTION: BOVINE ADENOVIRUS GENOME AND THEIR USE IN VACCINES
; FILE REFERENCE: 293102002121
; CURRENT APPLICATION NUMBER: US/09/103,330A
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 08/880,234
; EARLIER FILING DATE: 1997-06-23
; EARLIER APPLICATION NUMBER: 08/164,292
; EARLIER FILING DATE: 1993-12-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Bovine adenovirus type 3
; US-09-103-330-18

Query Match          56.2%; Score 36; DB 4; Length 308;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

Qy 2 YDPLTKLWL 10
|:|:|:|
Db 71 YNPTVLMWL 79

RESULT 36
US-09-435-242-18
; Sequence 18, Application US/09435242
; Patent No. 6379944
; GENERAL INFORMATION:
; APPLICANT: MITTAL, SURESH K.
; APPLICANT: GRAHAM, FRANK L.
; APPLICANT: PREVIC, LUDVIG
; APPLICANT: BABIUK, LORNE A.
; TITLE OF INVENTION: MAMMALIAN CELL LINES EXPRESSING BOVINE ADENOVIRUS FUNCTIONS
; FILE REFERENCE: 293102002102
; CURRENT APPLICATION NUMBER: US/09/435,242
; CURRENT FILING DATE: 1999-11-05
; EARLIER APPLICATION NUMBER: 08/815,927
; EARLIER FILING DATE: 1997-03-13
; EARLIER APPLICATION NUMBER: 08/164,294
; EARLIER FILING DATE: 1993-12-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 18
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Bovine adenovirus type 3
US-09-435-242-18

Query Match 56.2%; Score 36; DB 4; Length 308;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLWL 10
|:|:|:|
Db 71 YNPTVLMWL 79

RESULT 37
US-09-688-019-2
; Sequence 2, Application US/09688019
; Patent No. 6566512
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L.
; APPLICANT: Tinkelenberg, Arthur H.
; TITLE OF INVENTION: ARVI, A PROTEIN INVOLVED IN STEROL UPTAKE AND STEROL HOMEOSTASIS
; TITLE OF INVENTION: BUDDING YEAST, S. CEREVISIAE, AND A FUNCTIONAL HUMAN ARVI
; FILE REFERENCE: 0575/58072
; CURRENT APPLICATION NUMBER: US/09/688,019
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 2
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Human
US-09-688-019-2

Query Match 56.2%; Score 36; DB 4; Length 321;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLWL 10
|:|:|:|
Db 102 YDRNLRLMWL 110

RESULT 38
US-09-543-681A-5748
; Sequence 5748, Application US/09543681A
; Patent No. 6605709

; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5748
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5748

Query Match 56.2%; Score 36; DB 4; Length 364;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLWL 10
|:|:|:|
Db 200 YDPDKYWL 208

RESULT 39
US-09-491-577-36
; Sequence 36, Application US/09491577
; Patent No. 6610511
; GENERAL INFORMATION:
; APPLICANT: Yale University
; APPLICANT: Carlson, John R.
; APPLICANT: Kim, Hunhyong
; APPLICANT: Clyne, Peter J.
; APPLICANT: Warr, Coral G.
; TITLE OF INVENTION: No. 6610511el Family of Odorant Receptor Genes in Drosophila
; FILE REFERENCE: 44574-5061-US
; CURRENT APPLICATION NUMBER: US/09/491,577
; CURRENT FILING DATE: 2000-01-25
; EARLIER APPLICATION NUMBER: US 60/117,132
; EARLIER FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 36
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-491-577-36

Query Match 56.2%; Score 36; DB 4; Length 399;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10
|:|:|:|
Db 176 WHDGTLMWL 185

RESULT 40
US-09-134-000C-4382
; Sequence 4382, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentln version 3.1

SEQ ID NO 4382
LENGTH: 402
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-4382

Query Match 56.2%; Score 36; DB 4; Length 402;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 DPLTKLW 9
DB 232 DPLTKW 238

RESULT 41
US-09-107-532A-6726
Sequence 6726, Application US/09107532A
Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENCOM THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6726:

SEQUENCE CHARACTERISTICS:

LENGTH: 430 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHEtical: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1..430

SEQUENCE DESCRIPTION: SEQ ID NO: 6726:

US-09-107-532A-6726

Query Match 56.2%; Score 36; DB 4; Length 430;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 DPLTKLW 9
DB 250 DPLTKW 256

RESULT 42
US-09-134-000C-5803
Sequence 5803, Application US/09134000C
Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO 5803

LENGTH: 432

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-09-134-000C-5803

Query Match 56.2%; Score 36; DB 4; Length 432;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
DB 297 WYDPLTKIF 305

RESULT 43
US-09-914-259-13

Sequence 13, Application US/09914259

Patent No. 6495336

GENERAL INFORMATION:

APPLICANT: Makowski, Lee

APPLICANT: Hyman, Paul

APPLICANT: Williams, Mark

TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES

FILE REFERENCE: 8471-010-999

CURRENT APPLICATION NUMBER: US/09/914,259

CURRENT FILING DATE: 2000-11-21

NUMBER OF SEQ ID NOS: 180

SOFTWARE: FastSeq for windows Version 4.0

SEQ ID NO 13

LENGTH: 503

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-914-259-13

Query Match 56.2%; Score 36; DB 4; Length 503;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 10
DB 258 WYDPLTKRML 267

RESULT 44
US-09-543-681A-4359

Sequence 4359, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

US-09-543-681A-4359

PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4359
LENGTH: 641
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-4359

Query Match
Best Local Similarity 56.2%; Score 36; DB 4; Length 641;
Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKML 10
| | | | |
Db 253 YKPLDQJMW 261

RESULT 45
US-09-328-352-4365
Sequence 4365, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT FILING DATE: 1999-06-04
CURRENT APPLICATION NUMBER: US/09/328,352
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4365
LENGTH: 677
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4365

Query Match
Best Local Similarity 56.2%; Score 36; DB 4; Length 677;
Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLT 6
| | | | |
Db 232 WFDPLT 237

RESULT 46
US-08-931-952-2
Sequence 2, Application US/08931952
Patent No. 6054569
GENERAL INFORMATION:
APPLICANT: Bennett, Clark
APPLICANT: Laliberte, Maryse
APPLICANT: Gu, Kangfu
APPLICANT: Zimmerman, Joseph
APPLICANT: Tkalec, Lydia
APPLICANT: Danagher, Pamela
APPLICANT: Fink, Dominique
APPLICANT: Linhardt, Robert
TITLE OF INVENTION: CHONDROITIN LYASE ENZYMES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,952

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/272,247
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..23
OTHER INFORMATION: /note= "Amino acids 1 through 23
OTHER INFORMATION: are a leader peptide."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..700
OTHER INFORMATION: /note= "Amino acid sequence
OTHER INFORMATION: of chondroitinase AC from Flavobacterium
OTHER INFORMATION: heparinum."
US-08-931-952-2

Query Match
Best Local Similarity 56.2%; Score 36; DB 3; Length 700;
Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PLTKLM 9
| | | | |
Db 422 PLTKLM 427

RESULT 47
US-08-272-247-2
Sequence 2, Application US/08272247
Patent No. 6093563
GENERAL INFORMATION:
APPLICANT: Bennett, Clark
APPLICANT: Laliberte, Maryse
APPLICANT: Gu, Kangfu
APPLICANT: Zimmerman, Joseph
APPLICANT: Tkalec, Lydia
APPLICANT: Danagher, Pamela
APPLICANT: Fink, Dominique
APPLICANT: Linhardt, Robert
TITLE OF INVENTION: CHONDROITIN LYASE ENZYMES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/272,247
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: IT103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..23 /note="Amino acids 1 through 23
OTHER INFORMATION: are a leader peptide."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..700
OTHER INFORMATION: /note="Amino acid sequence
of chondroitinase AC from Flavobacterium
heparinum."
US-08-272-247-2
Query Match 56.2% Score 36; DB 3; Length 700;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PLTKLM 9
DB 422 PLTKLM 427
RESULT 48
PCT-US95-08560-2
Sequence 2, Application PC/TUS9508560
GENERAL INFORMATION:
APPLICANT: IBEX TECHNOLOGIES R AND D, INC.
TITLE OF INVENTION: CHONDROITIN LYASE ENZYMES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08560
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/272,247
FILING DATE: 08-Jun-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: IT103PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

FEATURE:
NAME/KEY: Peptide
LOCATION: 1..23 /note="Amino acids 1 through 23 are a leader
OTHER INFORMATION: peptide."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..700
OTHER INFORMATION: /note="Amino acid sequence
of chondroitinase AC from Flavobacterium
heparinum."
PCT-US95-08560-2

Query Match 56.2% Score 36; DB 5; Length 700;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PLTKLM 9
DB 422 PLTKLM 427

RESULT 49
US-09-540-236-3595
Sequence 3595, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARI
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540.236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3595
LENGTH: 713
TYPE: PRT
ORGANISM: M.cattarrhalis
US-09-540-236-3595

Query Match 56.2% Score 36; DB 4; Length 713;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLT 6
DB 271 WYDPLT 276

RESULT 50
US-09-688-188B-91
Sequence 91, Application US/09688188B
Patent No. 6656716
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0328
CURRENT APPLICATION NUMBER: US/09/688.188B
CURRENT FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 09/291,417
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 91
LENGTH: 842
TYPE: PRT
ORGANISM: Homo sapiens
US-09-688-188B-91

Query Match 56.2%; Score 36; DB 4; Length 842;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
||:|:|
Db 647 WYEPWQKFWL 656

RESULT 51
US-09-291-417D-91
; Sequence 91, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-91

Query Match 56.2%; Score 36; DB 4; Length 842;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
||:|:|
Db 647 WYEPWQKFWL 656

RESULT 52
US-09-543-681A-8019
; Sequence 8019, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 8019
; LENGTH: 1129
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-8019

Query Match 56.2%; Score 36; DB 4; Length 1129;
Best Local Similarity 62.5%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKL 8
||:|:|
Db 36 WYDPIINPL 43

RESULT 53
US-08-052-681-1
; Sequence 1, Application US/08052681
; Patent No. 5314819

GENERAL INFORMATION:
* APPLICANT: Kazuo YAMADA et al.
; TITLE OF INVENTION: NOVEL PROTEIN HAVING NITRILE HYDRATASE
; TITLE OF INVENTION: ACTIVITY AND THE GENE ENCODING THE SAME, AND A METHOD FOR PRODUCING THE SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/052,681
; FILING DATE: 19930427
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN: Rhizobium sp. MC12643
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLER:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:

DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-052-681-1

Query Match 54.7%; Score 35; DB 1; Length 198;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WYDPLTKML 10
Db 57 WTDPEFKKML 66

RESULT 54
US-09-252-991A-20618
Sequence 20618, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20618
LENGTH: 220
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-20618

Query Match 54.7%; Score 35; DB 4; Length 220;
Best Local Similarity 44.4%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKML 9
Db 11 WMSPTKGM 19

RESULT 55
US-09-150-133-11
Sequence 11, Application US/09150133B

GENERAL INFORMATION:
APPLICANT: The Board of Regents of the University of Oklahoma
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES, NUCLEIC ACIDS ENCODING
FILE REFERENCE: 5820.504
CURRENT APPLICATION NUMBER: US/09/150,133B
CURRENT FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 5.1 (saved in ASCII format)
SEQ ID NO 11
LENGTH: 359
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-150-133-11

Query Match 54.7%; Score 35; DB 3; Length 359;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DPLTKML 10
Db 171 DPTALML 178

RESULT 56
US-09-150-141-11
Sequence 11, Application US/09150141B

GENERAL INFORMATION:
APPLICANT: The Board of Regents of the University of Oklahoma
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES, NUCLEIC ACIDS ENCODING
FILE REFERENCE: 5820.495
CURRENT APPLICATION NUMBER: US/09/150,141B
CURRENT FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 5.1 (saved in ASCII format)
SEQ ID NO 11
LENGTH: 359
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-150-141-11

Query Match 54.7%; Score 35; DB 3; Length 359;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DPLTKML 10
Db 171 DPTALML 178

RESULT 57
US-09-374-493-11
Sequence 11, Application US/09374493

GENERAL INFORMATION:
APPLICANT: The Board of Regents of the University of Oklahoma
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
FILE REFERENCE: 5820.546
CURRENT APPLICATION NUMBER: US/09/374,493
CURRENT FILING DATE: 1999-08-13
EARLIER APPLICATION NUMBER: 09/150,133
EARLIER FILING DATE: 1998-09-09
EARLIER APPLICATION NUMBER: 60/072,994
EARLIER FILING DATE: 1998-01-29
EARLIER APPLICATION NUMBER: PCT/US99/16750
EARLIER FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 8.0 (saved in ASCII format)
SEQ ID NO 11
LENGTH: 359
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-374-493-11

Query Match 54.7%; Score 35; DB 3; Length 359;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DPLTKML 10
Db 171 DPTALML 178

RESULT 58
US-09-374-824-11
Sequence 11, Application US/09374824

GENERAL INFORMATION:
APPLICANT: The Board of Regents of the University of Oklahoma
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
FILE REFERENCE: 5820.547
CURRENT APPLICATION NUMBER: US/09/374,824
CURRENT FILING DATE: 1999-08-13
EARLIER APPLICATION NUMBER: 09/150,133

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; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 60/072,994
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: PCT/US99/16750
; EARLIER FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Wordperfect 8.0 (saved in ASCII format)
; SEQ ID NO 11
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-374-824-11

Query Match
Best Local Similarity 54.7%; Score 35; DB 3; Length 359;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DPLTKLWL 10
Db 171 DPTLWL 178

RESULT 59
US-09-374-492-11
; Sequence 11, Application US/09374492
; Patent No. 6207432
; GENERAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Oklahoma
; TITLE OF INVENTION: TYROSYLPHOEPTIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
; FILE REFERENCE: 5820.545
; CURRENT FILING DATE: 1999-08-13
; EARLIER APPLICATION NUMBER: 09/150,141
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 60/072,994
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: PCT/US99/16750
; EARLIER FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Wordperfect 8.0 (saved in ASCII format)
; SEQ ID NO 11
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-374-492-11

Query Match
Best Local Similarity 54.7%; Score 35; DB 3; Length 359;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DPLTKLWL 10
Db 171 DPTLWL 178

RESULT 60
US-09-785-343-11
; Sequence 11, Application US/09785343
; Patent No. 6605455
; GENERAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Oklahoma
; TITLE OF INVENTION: TYROSYLPHOEPTIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
; FILE REFERENCE: 5827.003
; CURRENT FILING DATE: 2001-02-16
; EARLIER APPLICATION NUMBER: 09/150,133
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 60/072,994
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: PCT/US99/16750
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Wordperfect 8.0 (saved in ASCII format)
```

```
; SEQ ID NO 11
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-785-343-11

Query Match
Best Local Similarity 54.7%; Score 35; DB 4; Length 359;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DPLTKLWL 10
Db 171 DPTLWL 178

RESULT 61
US-09-724-566A-75
; Sequence 75, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basl, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT FILING DATE: 2000-11-28
; EARLIER APPLICATION NUMBER: US/09/724,566A
; EARLIER FILING DATE: 2000-02-10
; EARLIER APPLICATION NUMBER: US 09/501,708
; EARLIER FILING DATE: 2000-02-10
; EARLIER APPLICATION NUMBER: 60/119,571
; EARLIER FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 60/139,172
; EARLIER FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-75

Query Match
Best Local Similarity 54.7%; Score 35; DB 4; Length 361;
Best Local Similarity 44.4%; Pred. No. 3.3e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
Db 188 WYPIRREW 196

RESULT 62
US-09-724-566A-71
; Sequence 71, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basl, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
```

```
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
FILE REFERENCE: 228-US-NEWC2
CURRENT FILING DATE: 2000-11-28
CURRENT APPLICATION NUMBER: US/09/724,566A
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 71
LENGTH: 374
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-566A-71
```

```
Query Match          54.7%; Score 35; DB 4; Length 374;
Best Local Similarity 44.4%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 WYDPLTKLM 9
      |||:|:|
Db      205 WYTPIRREW 213
```

```
RESULT 63
US-09-724-566A-70
Sequence 70, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basl, Gurigbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 70
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-566A-70
```

```
Query Match          54.7%; Score 35; DB 4; Length 390;
Best Local Similarity 44.4%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 WYDPLTKLM 9
      |||:|:|
Db      188 WYTPIRREW 196
```

```
RESULT 64
US-09-724-566A-68
Sequence 68, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basl, Gurigbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 68
LENGTH: 395
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-566A-68
```

```
Query Match          54.7%; Score 35; DB 4; Length 395;
Best Local Similarity 44.4%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 WYDPLTKLM 9
      |||:|:|
Db      193 WYTPIRREW 201
```

```
RESULT 65
US-09-724-566A-58
Sequence 58, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basl, Gurigbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-58
```

```
Query Match          54.7%; Score 35; DB 4; Length 407;
Best Local Similarity 44.4%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      1 WYDPLTKLM 9
        |||:|:|
Db      205 WYTPIRREW 213
```

```
RESULT 66
US-09-724-566A-57
; Sequence 57, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
```

```
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-57
```

```
Query Match          54.7%; Score 35; DB 4; Length 419;
Best Local Similarity 44.4%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      1 WYDPLTKLM 9
        |||:|:|
Db      250 WYTPIRREW 258
```

```
RESULT 67
US-09-724-566A-60
; Sequence 60, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
```

```
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-60
```

```
Query Match          54.7%; Score 35; DB 4; Length 420;
Best Local Similarity 44.4%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      1 WYDPLTKLM 9
        |||:|:|
Db      250 WYTPIRREW 258
```

```
RESULT 68
US-08-879-337-5
; Sequence 5, Application US/08879337B
; Patent No. 6639130
; GENERAL INFORMATION:
; APPLICANT: Jang, Jyan-Chyun
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
; FILE REFERENCE: 00786/338001
; CURRENT APPLICATION NUMBER: US/08/879,337B
; CURRENT FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/022,086
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-08-879-337-5
```

```
Query Match          54.7%; Score 35; DB 4; Length 424;
Best Local Similarity 55.6%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      1 WYDPLTKLM 9
        |||:|:|
Db      72 WFTLTLLM 80
```

```
RESULT 69
US-09-548-372D-28
; Sequence 28, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
```

```

; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 28
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-28
```

```

Query Match          54.7%; Score 35; DB 4; Length 425;
Best Local Similarity 44.4%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLM 9
|||:|
Db      222 WYPIRREW 230
```

```

RESULT 70
US-09-548-367D-28
; Sequence 28, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 28
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-28
```

```

Query Match          54.7%; Score 35; DB 4; Length 425;
Best Local Similarity 44.4%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLM 9
|||:|
Db      222 WYPIRREW 230
```

```

RESULT 71
US-09-551-853D-28
; Sequence 28, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
```

```

; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 28
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-28
```

```

Query Match          54.7%; Score 35; DB 4; Length 425;
Best Local Similarity 44.4%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLM 9
|||:|
Db      222 WYPIRREW 230
```

```

RESULT 72
US-09-548-372D-51
; Sequence 51, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 51
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Aep2 (b) delta TM
US-09-548-372D-51
```

```

Query Match          54.7%; Score 35; DB 4; Length 428;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLM 9
|||:|
Db      225 WYPIRREW 233
```

```

RESULT 73
US-09-548-367D-51
; Sequence 51, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
```

```

; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 51
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2 (b) delta TM
US-09-548-367D-51

Query Match          54.7%; Score 35; DB 4; Length 428;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
Db 225 WYTPIRREW 233

RESULT 74
US-09-551-853D-51
; Sequence 51, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 51
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2 (b) delta TM
US-09-551-853D-51

Query Match          54.7%; Score 35; DB 4; Length 428;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
Db 225 WYTPIRREW 233

RESULT 75
US-09-724-566A-74
; Sequence 74, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Baesi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
```

```

; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEMC2
; CURRENT FILING DATE: US/09/724,566A
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-74

Query Match          54.7%; Score 35; DB 4; Length 431;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
Db 229 WYTPIRREW 237

RESULT 76
US-09-548-372D-26
; Sequence 26, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280I
; CURRENT FILING DATE: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-26

Query Match          54.7%; Score 35; DB 4; Length 433;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
Db 230 WYTPIRREW 238

RESULT 77
US-09-548-367D-26
```

```
; Sequence 26, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-26
```

```
Query Match          54.7%; Score 35; DB 4; Length 433;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLW 9
Db      230 WYTPIRREW 238
```

```
RESULT 78
US-09-551-853D-26
; Sequence 26, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-26
```

```
Query Match          54.7%; Score 35; DB 4; Length 433;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLW 9
Db      230 WYTPIRREW 238
```

```
RESULT 79
US-09-548-372D-53
; Sequence 53, Application US/09548372D
```

```
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 53
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-372D-53
```

```
Query Match          54.7%; Score 35; DB 4; Length 434;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLW 9
Db      225 WYTPIRREW 233
```

```
RESULT 80
US-09-548-367D-53
; Sequence 53, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 53
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-367D-53
```

```
Query Match          54.7%; Score 35; DB 4; Length 434;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLW 9
Db      225 WYTPIRREW 233
```



```
RESULT 81
US-09-551-853D-53
; Sequence 53, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2 (D) delta TM
US-09-551-853D-53

Query Match          54.7%; Score 35; DB 4; Length 434;
Best Local Similarity 44.4%; Pred. NO. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 WYDPLTKLM 9
Db      225 WYPIRREW 233

RESULT 82
US-09-724-566A-69
; Sequence 69, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-69
```

```
Query Match          54.7%; Score 35; DB 4; Length 439;
Best Local Similarity 44.4%; Pred. NO. 4.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 WYDPLTKLM 9
Db      188 WYPIRREW 196

RESULT 83
US-09-724-566A-67
; Sequence 67, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-67

Query Match          54.7%; Score 35; DB 4; Length 444;
Best Local Similarity 44.4%; Pred. NO. 4.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 WYDPLTKLM 9
Db      193 WYPIRREW 201

RESULT 84
US-09-548-372D-22
; Sequence 22, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
```

SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 446
TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-372D-22

Query Match 54.7%; Score 35; DB 4; Length 446;
Best Local Similarity 44.4%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
DB 243 WYTPIRREW 251

RESULT 85
US-09-548-367D-22
Sequence 22, Application US/09548367D
Patent No. 6440698

GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE REFERENCE: 29915/6280H
CURRENT APPLICATION NUMBER: US/09/548,367D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 446
TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-367D-22

Query Match 54.7%; Score 35; DB 4; Length 446;
Best Local Similarity 44.4%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
DB 243 WYTPIRREW 251

RESULT 86
US-09-551-853D-22
Sequence 22, Application US/09551853D
Patent No. 6500667
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE REFERENCE: 29915/6280L
CURRENT APPLICATION NUMBER: US/09/551,853D
CURRENT FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1

SEQ ID NO 22
LENGTH: 446
TYPE: PRT
ORGANISM: Homo sapiens
US-09-551-853D-22

Query Match 54.7%; Score 35; DB 4; Length 446;
Best Local Similarity 44.4%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
DB 243 WYTPIRREW 251

RESULT 87
US-09-230-371A-28
Sequence 28, Application US/09230371A
Patent No. 6348586

GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bonenzky, Roy A
APPLICANT: Russo, James J
APPLICANT: Edelman, Isidore S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
FILE REFERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1997-07-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 449
TYPE: PRT
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-28

Query Match 54.7%; Score 35; DB 4; Length 449;
Best Local Similarity 85.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PLTKLML 10
DB 398 PLVRLWL 404

RESULT 88
US-09-724-566A-59
Sequence 59, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basi, Gurigbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Jonn, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
FILE REFERENCE: 228-US-NEMC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571

;; PRIOR FILING DATE: 1999-02-10
;; PRIOR APPLICATION NUMBER: 60/139,172
;; PRIOR FILING DATE: 1999-06-15
;; NUMBER OF SEQ ID NOS: 104
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 59
;; LENGTH: 452
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-724-566A-59

Query Match 54.7%; Score 35; DB 4; Length 453;
Best Local Similarity 44.4%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
|||:|
Db 250 WYTPIRREW 258

RESULT 89
US-09-548-372D-30
; Sequence 30, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-30

Query Match 54.7%; Score 35; DB 4; Length 453;
Best Local Similarity 44.4%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
|||:|
Db 250 WYTPIRREW 258

RESULT 90
US-09-548-367D-30
; Sequence 30, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23

;; PRIOR APPLICATION NUMBER: US 60/101,594
;; PRIOR FILING DATE: 1998-09-24
;; NUMBER OF SEQ ID NOS: 73
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 30
;; LENGTH: 453
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-548-367D-30

Query Match 54.7%; Score 35; DB 4; Length 453;
Best Local Similarity 44.4%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
|||:|
Db 250 WYTPIRREW 258

RESULT 91
US-09-551-853D-30
; Sequence 30, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-30

Query Match 54.7%; Score 35; DB 4; Length 453;
Best Local Similarity 44.4%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
|||:|
Db 250 WYTPIRREW 258

RESULT 92
US-09-724-566A-43
; Sequence 43, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods

FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 43
LENGTH: 456
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-566A-43

Query Match 54.7%; Score 35; DB 4; Length 456;
Best Local Similarity 44.4%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9
|||:|
Db 205 WYTPIRREW 213

RESULT 93
US-09-548-372D-24
Sequence 24, Application US/09548372D
Patent No. 6420534
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US/09/548,372D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 459
TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-372D-24

Query Match 54.7%; Score 35; DB 4; Length 459;
Best Local Similarity 44.4%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9
|||:|
Db 256 WYTPIRREW 264

RESULT 94
US-09-548-372D-32
Sequence 32, Application US/09548372D
Patent No. 6420534
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US/09/548,372D
CURRENT FILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
LENGTH: 459
TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-372D-32

Query Match 54.7%; Score 35; DB 4; Length 459;
Best Local Similarity 44.4%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9
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Db 250 WYTPIRREW 258

RESULT 95
US-09-548-367D-24
Sequence 24, Application US/09548367D
Patent No. 6440698
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US/09/548,367D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 459
TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-367D-24

Query Match 54.7%; Score 35; DB 4; Length 459;
Best Local Similarity 44.4%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 256 WYTPIRREW 264

RESULT 96
US-09-548-367D-32
Sequence 32, Application US/09548367D
Patent No. 6440698
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US/09/548,367D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
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; ORGANISM: Homo sapiens
US-09-548-367D-32

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Best Local Similarity 44.4%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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; Sequence 24, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
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US-09-551-853D-24

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; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23

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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
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US-09-551-853D-32

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; Patent No. 6420534
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; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
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US-09-548-372D-6

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Best Local Similarity 44.4%; Pred. No. 4.4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133

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us-09-932-613-457.ra1

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; PRIOR FILING DATE: 1999-09-23
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Db 225 WYTPIRREW 233

Search completed: July 12, 2004, 21:30:18
Job time : 26 secs

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OM protein - protein search, using sw model

Run on: July 12, 2004, 21:29:57 ; Search time 46 Seconds

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Title: US-09-932-613-457

Perfect score: 64

Sequence: 1 WYDPLTKML 10

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SUMMARIES

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128	64	100.0	14	10	US-09-932-322-193	Sequence 193, App	201	64	100.0	14	10	US-09-932-322-266	Sequence 266, App
129	64	100.0	14	10	US-09-932-322-194	Sequence 194, App	202	64	100.0	14	10	US-09-932-322-267	Sequence 267, App
130	64	100.0	14	10	US-09-932-322-195	Sequence 195, App	203	64	100.0	14	10	US-09-932-322-268	Sequence 268, App
131	64	100.0	14	10	US-09-932-322-196	Sequence 196, App	204	64	100.0	14	10	US-09-932-322-269	Sequence 269, App
132	64	100.0	14	10	US-09-932-322-197	Sequence 197, App	205	64	100.0	14	10	US-09-932-322-270	Sequence 270, App
133	64	100.0	14	10	US-09-932-322-198	Sequence 198, App	206	64	100.0	14	10	US-09-932-322-271	Sequence 271, App
134	64	100.0	14	10	US-09-932-322-199	Sequence 199, App	207	64	100.0	14	10	US-09-932-322-272	Sequence 272, App
135	64	100.0	14	10	US-09-932-322-200	Sequence 200, App	208	64	100.0	14	10	US-09-932-322-273	Sequence 273, App
136	64	100.0	14	10	US-09-932-322-201	Sequence 201, App	209	64	100.0	14	10	US-09-932-322-274	Sequence 274, App
137	64	100.0	14	10	US-09-932-322-202	Sequence 202, App	210	64	100.0	14	10	US-09-932-322-275	Sequence 275, App
138	64	100.0	14	10	US-09-932-322-203	Sequence 203, App	211	64	100.0	14	10	US-09-932-322-276	Sequence 276, App
139	64	100.0	14	10	US-09-932-322-204	Sequence 204, App	212	64	100.0	14	10	US-09-932-322-277	Sequence 277, App
140	64	100.0	14	10	US-09-932-322-205	Sequence 205, App	213	64	100.0	14	10	US-09-932-322-278	Sequence 278, App
141	64	100.0	14	10	US-09-932-322-206	Sequence 206, App	214	64	100.0	14	10	US-09-932-322-279	Sequence 279, App
142	64	100.0	14	10	US-09-932-322-207	Sequence 207, App	215	64	100.0	14	10	US-09-932-322-280	Sequence 280, App
143	64	100.0	14	10	US-09-932-322-208	Sequence 208, App	216	64	100.0	14	10	US-09-932-322-281	Sequence 281, App
144	64	100.0	14	10	US-09-932-322-209	Sequence 209, App	217	64	100.0	14	10	US-09-932-322-282	Sequence 282, App
145	64	100.0	14	10	US-09-932-322-210	Sequence 210, App	218	64	100.0	14	10	US-09-932-322-283	Sequence 283, App
146	64	100.0	14	10	US-09-932-322-211	Sequence 211, App	219	64	100.0	14	10	US-09-932-322-284	Sequence 284, App
147	64	100.0	14	10	US-09-932-322-212	Sequence 212, App	220	64	100.0	14	10	US-09-932-322-285	Sequence 285, App
148	64	100.0	14	10	US-09-932-322-213	Sequence 213, App	221	64	100.0	14	10	US-09-932-322-286	Sequence 286, App
149	64	100.0	14	10	US-09-932-322-214	Sequence 214, App	222	64	100.0	14	10	US-09-932-322-287	Sequence 287, App
150	64	100.0	14	10	US-09-932-322-215	Sequence 215, App	223	64	100.0	14	10	US-09-932-322-288	Sequence 288, App
151	64	100.0	14	10	US-09-932-322-216	Sequence 216, App	224	64	100.0	14	10	US-09-932-322-289	Sequence 289, App
152	64	100.0	14	10	US-09-932-322-217	Sequence 217, App	225	64	100.0	14	10	US-09-932-322-290	Sequence 290, App
153	64	100.0	14	10	US-09-932-322-218	Sequence 218, App	226	64	100.0	14	10	US-09-932-322-291	Sequence 291, App
154	64	100.0	14	10	US-09-932-322-219	Sequence 219, App	227	64	100.0	14	10	US-09-932-322-292	Sequence 292, App
155	64	100.0	14	10	US-09-932-322-220	Sequence 220, App	228	64	100.0	14	10	US-09-932-322-293	Sequence 293, App
156	64	100.0	14	10	US-09-932-322-221	Sequence 221, App	229	64	100.0	14	10	US-09-932-322-294	Sequence 294, App
157	64	100.0	14	10	US-09-932-322-222	Sequence 222, App	230	64	100.0	14	10	US-09-932-322-295	Sequence 295, App
158	64	100.0	14	10	US-09-932-322-223	Sequence 223, App	231	64	100.0	14	10	US-09-932-322-296	Sequence 296, App
159	64	100.0	14	10	US-09-932-322-224	Sequence 224, App	232	64	100.0	14	10	US-09-932-322-297	Sequence 297, App
160	64	100.0	14	10	US-09-932-322-225	Sequence 225, App	233	64	100.0	15	10	US-09-932-322-298	Sequence 298, App
161	64	100.0	14	10	US-09-932-322-226	Sequence 226, App	234	64	100.0	15	10	US-09-932-322-299	Sequence 299, App

235	64	100.0	17	10	US-09-932-613-437	Sequence 437, App
236	64	100.0	17	10	US-09-932-613-440	Sequence 440, App
237	64	100.0	17	10	US-09-932-613-437	Sequence 437, App
238	64	100.0	17	10	US-09-932-613-440	Sequence 440, App
239	62	96.9	14	10	US-09-932-613-385	Sequence 385, App
240	62	96.9	14	10	US-09-932-613-386	Sequence 386, App
241	62	96.9	14	10	US-09-932-613-387	Sequence 387, App
242	62	96.9	14	10	US-09-932-613-388	Sequence 388, App
243	62	96.9	14	10	US-09-932-613-389	Sequence 389, App
244	62	96.9	14	10	US-09-932-613-390	Sequence 390, App
245	62	96.9	14	10	US-09-932-613-385	Sequence 385, App
246	62	96.9	14	10	US-09-932-613-386	Sequence 386, App
247	62	96.9	14	10	US-09-932-613-387	Sequence 387, App
248	62	96.9	14	10	US-09-932-613-388	Sequence 388, App
249	62	96.9	14	10	US-09-932-613-389	Sequence 389, App
250	62	96.9	14	10	US-09-932-613-390	Sequence 390, App
251	61	95.3	14	10	US-09-932-613-375	Sequence 375, App
252	61	95.3	14	10	US-09-932-613-376	Sequence 376, App
253	61	95.3	14	10	US-09-932-613-377	Sequence 377, App
254	61	95.3	14	10	US-09-932-613-378	Sequence 378, App
255	61	95.3	14	10	US-09-932-613-379	Sequence 379, App
256	61	95.3	14	10	US-09-932-613-380	Sequence 380, App
257	61	95.3	14	10	US-09-932-613-381	Sequence 381, App
258	61	95.3	14	10	US-09-932-613-382	Sequence 382, App
259	61	95.3	14	10	US-09-932-613-383	Sequence 383, App
260	61	95.3	14	10	US-09-932-613-384	Sequence 384, App
261	61	95.3	14	10	US-09-932-613-375	Sequence 375, App
262	61	95.3	14	10	US-09-932-613-376	Sequence 376, App
263	61	95.3	14	10	US-09-932-613-377	Sequence 377, App
264	61	95.3	14	10	US-09-932-613-378	Sequence 378, App
265	61	95.3	14	10	US-09-932-613-379	Sequence 379, App
266	61	95.3	14	10	US-09-932-613-380	Sequence 380, App
267	61	95.3	14	10	US-09-932-613-381	Sequence 381, App
268	61	95.3	14	10	US-09-932-613-382	Sequence 382, App
269	61	95.3	14	10	US-09-932-613-383	Sequence 383, App
270	61	95.3	14	10	US-09-932-613-384	Sequence 384, App
271	60	93.8	14	10	US-09-932-613-306	Sequence 306, App
272	60	93.8	14	10	US-09-932-613-307	Sequence 307, App
273	60	93.8	14	10	US-09-932-613-308	Sequence 308, App
274	60	93.8	14	10	US-09-932-613-309	Sequence 309, App
275	60	93.8	14	10	US-09-932-613-310	Sequence 310, App
276	60	93.8	14	10	US-09-932-613-311	Sequence 311, App
277	60	93.8	14	10	US-09-932-613-312	Sequence 312, App
278	60	93.8	14	10	US-09-932-613-313	Sequence 313, App
279	60	93.8	14	10	US-09-932-613-314	Sequence 314, App
280	60	93.8	14	10	US-09-932-613-315	Sequence 315, App
281	60	93.8	14	10	US-09-932-613-316	Sequence 316, App
282	60	93.8	14	10	US-09-932-613-317	Sequence 317, App
283	60	93.8	14	10	US-09-932-613-318	Sequence 318, App
284	60	93.8	14	10	US-09-932-613-319	Sequence 319, App
285	60	93.8	14	10	US-09-932-613-320	Sequence 320, App
286	60	93.8	14	10	US-09-932-613-321	Sequence 321, App
287	60	93.8	14	10	US-09-932-613-322	Sequence 322, App
288	60	93.8	14	10	US-09-932-613-323	Sequence 323, App
289	60	93.8	14	10	US-09-932-613-352	Sequence 352, App
290	60	93.8	14	10	US-09-932-613-353	Sequence 353, App
291	60	93.8	14	10	US-09-932-613-354	Sequence 354, App
292	60	93.8	14	10	US-09-932-613-355	Sequence 355, App
293	60	93.8	14	10	US-09-932-613-356	Sequence 356, App
294	60	93.8	14	10	US-09-932-613-357	Sequence 357, App
295	60	93.8	14	10	US-09-932-613-358	Sequence 358, App
296	60	93.8	14	10	US-09-932-613-359	Sequence 359, App
297	60	93.8	14	10	US-09-932-613-360	Sequence 360, App
298	60	93.8	14	10	US-09-932-613-361	Sequence 361, App
299	60	93.8	14	10	US-09-932-613-362	Sequence 362, App
300	60	93.8	14	10	US-09-932-613-363	Sequence 363, App

ALIGNMENTS

```
Sequence 436, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DXX-025.1 PCT; DXX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 436
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: core peptide of high affinity Blys binders
US-09-932-613-436
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Query Match          100.0%; Score 64; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 WYDPLTKLML 10
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Db       1 WYDPLTKLML 10
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RESULT 2
US-09-932-613-457
; Sequence 457, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DXX-025.1 PCT; DXX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 457
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-457
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Query Match          100.0%; Score 64; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 WYDPLTKLML 10
        |||||
Db       1 WYDPLTKLML 10
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RESULT 3
US-09-932-322-436
; Sequence 436, Application US/09932322
; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
```

```

; APPLICANT: Ladner, Robert Charles
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (Blys)
; FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
; CURRENT APPLICATION NUMBER: US/09/932,322
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 436
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: core peptide of high affinity Blys binders
US-09-932-322-436

Query Match          100.0%; Score 64; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLWL 10
        |||||
        1 WYDPLTKLWL 10

DB      1 WYDPLTKLWL 10

RESULT 4
US-09-932-322-457
; Sequence 457, Application US/09932322
; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Belzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (Blys)
; FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
; CURRENT APPLICATION NUMBER: US/09/932,322
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 457
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-322-457

Query Match          100.0%; Score 64; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLWL 10
        |||||
        1 WYDPLTKLWL 10

DB      1 WYDPLTKLWL 10

RESULT 5
US-09-932-613-456
; Sequence 456, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
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; SEQ ID NO 456
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-456

Query Match          100.0%; Score 64; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLWL 10
        |||||
        1 WYDPLTKLWL 10

DB      1 WYDPLTKLWL 10

RESULT 6
US-09-932-322-456
; Sequence 456, Application US/09932322
; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Belzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Ladner, Robert Charles
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (Blys)
; FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
; CURRENT APPLICATION NUMBER: US/09/932,322
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 456
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-322-456

Query Match          100.0%; Score 64; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLWL 10
        |||||
        1 WYDPLTKLWL 10

DB      1 WYDPLTKLWL 10

RESULT 7
US-09-932-613-439
; Sequence 439, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 439
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-439
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Query Match 100.0%; Score 64; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
|||||
Db 1 WYDPLTKLML 10

RESULT 8
US-09-932-322-439
; Sequence 439, Application US/09932322
; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Laderer, Robert Charles
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (Blys)
; FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
; CURRENT APPLICATION NUMBER: US/09/932.322
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 439
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-322-439

Query Match 100.0%; Score 64; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
|||||
Db 1 WYDPLTKLML 10

RESULT 9
US-09-932-613-186
; Sequence 186, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932.613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 186
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-186

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
|||||
Db 1 WYDPLTKLML 10

Db 3 WYDPLTKLML 12

RESULT 10
US-09-932-613-187
; Sequence 187, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932.613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 187
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-187

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
|||||
Db 3 WYDPLTKLML 12

RESULT 11
US-09-932-613-188
; Sequence 188, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932.613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 188
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-188

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
|||||
Db 3 WYDPLTKLML 12

RESULT 12
US-09-932-613-189
; Sequence 189, Application US/09932613
; Publication No. US20030091565A1

```

; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltez, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dlx-025.1 PCT; Dlx-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 189
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-189

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
   |||||
Db 3 WYDPLTKLWL 12

RESULT 13
US-09-932-613-190
; Sequence 190, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltez, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dlx-025.1 PCT; Dlx-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 190
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-190

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
   |||||
Db 3 WYDPLTKLWL 12

RESULT 14
US-09-932-613-191
; Sequence 191, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltez, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
```

```

; FILE REFERENCE: Dlx-025.1 PCT; Dlx-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 191
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-191

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
   |||||
Db 3 WYDPLTKLWL 12

RESULT 15
US-09-932-613-192
; Sequence 192, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltez, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dlx-025.1 PCT; Dlx-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 192
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-192

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
   |||||
Db 3 WYDPLTKLWL 12

RESULT 16
US-09-932-613-193
; Sequence 193, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltez, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dlx-025.1 PCT; Dlx-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 193
; LENGTH: 14
```

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-193

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|||
Db 3 WYDPLTKLWL 12

RESULT 17
US-09-932-613-194
Sequence 194, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 194
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-194

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|||
Db 3 WYDPLTKLWL 12

RESULT 18
US-09-932-613-195
Sequence 195, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 195
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-195

Query Match 100.0%; Score 64; DB 10; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|||
Db 3 WYDPLTKLWL 12

RESULT 19
US-09-932-613-196
Sequence 196, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 196
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-196

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|||
Db 3 WYDPLTKLWL 12

RESULT 20
US-09-932-613-197
Sequence 197, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 197
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-197

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|||
Db 3 WYDPLTKLWL 12

RESULT 21
US-09-932-613-198
; Sequence 198, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 198
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-198

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
 |||||
DB 3 WYDPLTKLML 12

RESULT 22
US-09-932-613-199
; Sequence 199, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 199
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-199

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
 |||||
DB 3 WYDPLTKLML 12

RESULT 23
US-09-932-613-200
; Sequence 200, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.

; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 200
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-200

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
 |||||
DB 3 WYDPLTKLML 12

RESULT 24
US-09-932-613-201
; Sequence 201, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 201
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-201

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
 |||||
DB 3 WYDPLTKLML 12

RESULT 25
US-09-932-613-202
; Sequence 202, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613

```

; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
; US-09-932-613-204
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 202
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
; US-09-932-613-202

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
    |||||
    |||||
Db 3 WYDPLTKLML 12

RESULT 26
US-09-932-613-203
; Sequence 203, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 203
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
; US-09-932-613-203

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
    |||||
    |||||
Db 3 WYDPLTKLML 12

RESULT 27
US-09-932-613-204
; Sequence 204, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 204
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```

; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
; US-09-932-613-204
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 202
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
; US-09-932-613-202

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
    |||||
    |||||
Db 3 WYDPLTKLML 12

RESULT 28
US-09-932-613-205
; Sequence 205, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 205
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
; US-09-932-613-205

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
    |||||
    |||||
Db 3 WYDPLTKLML 12

RESULT 29
US-09-932-613-206
; Sequence 206, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 206
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
; US-09-932-613-206

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 WYDPLTKLML 10
| | | | |
Db 3 WYDPLTKLML 12

RESULT 30
US-09-932-613-207
; Sequence 207, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 207
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-207

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
| | | | |
Db 3 WYDPLTKLML 12

RESULT 31
US-09-932-613-208
; Sequence 208, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 208
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-208

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
| | | | |
Db 3 WYDPLTKLML 12

RESULT 32

US-09-932-613-209
; Sequence 209, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 209
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-209

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
| | | | |
Db 3 WYDPLTKLML 12

RESULT 33
US-09-932-613-210
; Sequence 210, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 210
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-210

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
| | | | |
Db 3 WYDPLTKLML 12

RESULT 34
US-09-932-613-211
; Sequence 211, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel


```

; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 211
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-211

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLML 10
        |||||
        3 WYDPLTKLML 12

RESULT 35
US-09-932-613-212
; Sequence 212, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 212
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-212

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLML 10
        |||||
        3 WYDPLTKLML 12

RESULT 36
US-09-932-613-213
; Sequence 213, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 213
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
```

```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 213
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-213

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLML 10
        |||||
        3 WYDPLTKLML 12

RESULT 37
US-09-932-613-214
; Sequence 214, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 214
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-214

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLML 10
        |||||
        3 WYDPLTKLML 12

RESULT 38
US-09-932-613-215
; Sequence 215, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 215
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
```

US-09-932-613-215

Query Match
Best Local Similarity 100.0%; Score 64; DB 10; Length 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|||||
3 WYDPLTKLWL 12

RESULT 39

US-09-932-613-216
; Sequence 216, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 216
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-216

Query Match
Best Local Similarity 100.0%; Score 64; DB 10; Length 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|||||
3 WYDPLTKLWL 12

RESULT 40

US-09-932-613-217
; Sequence 217, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 217
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-217

Query Match
Best Local Similarity 100.0%; Score 64; DB 10; Length 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10

Db 3 WYDPLTKLWL 12
|||||

RESULT 41
US-09-932-613-218
; Sequence 218, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 218
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-218

Query Match
Best Local Similarity 100.0%; Score 64; DB 10; Length 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|||||
3 WYDPLTKLWL 12

RESULT 42
US-09-932-613-219
; Sequence 219, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 219
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-219

Query Match
Best Local Similarity 100.0%; Score 64; DB 10; Length 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|||||
3 WYDPLTKLWL 12

RESULT 43
US-09-932-613-220
; Sequence 220, Application US/09932613

```

; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 220
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-220

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLML 10
        |||||
Db      3 WYDPLTKLML 12

RESULT 44
US-09-932-613-221
; Sequence 221, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 221
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-221

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLML 10
        |||||
Db      3 WYDPLTKLML 12

RESULT 45
US-09-932-613-222
; Sequence 222, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
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```

; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 222
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-222

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLML 10
        |||||
Db      3 WYDPLTKLML 12

RESULT 46
US-09-932-613-223
; Sequence 223, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 223
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-223

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLML 10
        |||||
Db      3 WYDPLTKLML 12

RESULT 47
US-09-932-613-224
; Sequence 224, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 224
```

LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Blys binding polypeptide
 US-09-932-613-224

Query Match 100.0%; Score 64; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 |||||
 DB 3 WYDPLTKLWL 12

RESULT 48
 US-09-932-613-225
 Sequence 225, Application US/09932613
 Publication No. US20030091565A1
 GENERAL INFORMATION:
 APPLICANT: Human Genome Sciences, Inc.
 APPLICANT: Beltzer, James P.
 APPLICANT: Potter, M. Daniel
 APPLICANT: Fleming, Tony J.
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
 FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
 CURRENT FILING DATE: 2001-08-17
 NUMBER OF SEQ ID NOS: 458
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 225
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Blys binding polypeptide
 US-09-932-613-225

Query Match 100.0%; Score 64; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 |||||
 DB 3 WYDPLTKLWL 12

RESULT 49
 US-09-932-613-226
 Sequence 226, Application US/09932613
 Publication No. US20030091565A1
 GENERAL INFORMATION:
 APPLICANT: Human Genome Sciences, Inc.
 APPLICANT: Beltzer, James P.
 APPLICANT: Potter, M. Daniel
 APPLICANT: Fleming, Tony J.
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
 FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
 CURRENT FILING DATE: 2001-08-17
 NUMBER OF SEQ ID NOS: 458
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 226
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Blys binding polypeptide
 US-09-932-613-226

Query Match 100.0%; Score 64; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 |||||
 DB 3 WYDPLTKLWL 12

RESULT 50
 US-09-932-613-227
 Sequence 227, Application US/09932613
 Publication No. US20030091565A1
 GENERAL INFORMATION:
 APPLICANT: Human Genome Sciences, Inc.
 APPLICANT: Beltzer, James P.
 APPLICANT: Potter, M. Daniel
 APPLICANT: Fleming, Tony J.
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
 FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
 CURRENT FILING DATE: 2001-08-17
 NUMBER OF SEQ ID NOS: 458
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 227
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Blys binding polypeptide
 US-09-932-613-227

Query Match 100.0%; Score 64; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 |||||
 DB 3 WYDPLTKLWL 12

RESULT 51
 US-09-932-613-228
 Sequence 228, Application US/09932613
 Publication No. US20030091565A1
 GENERAL INFORMATION:
 APPLICANT: Human Genome Sciences, Inc.
 APPLICANT: Beltzer, James P.
 APPLICANT: Potter, M. Daniel
 APPLICANT: Fleming, Tony J.
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
 FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
 CURRENT FILING DATE: 2001-08-17
 NUMBER OF SEQ ID NOS: 458
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 228
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Blys binding polypeptide
 US-09-932-613-228

Query Match 100.0%; Score 64; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 |||||
 DB 3 WYDPLTKLWL 12

```
RESULT 52
US-09-932-613-229
; Sequence 229, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 229
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-229

Query Match      100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 53
US-09-932-613-230
; Sequence 230, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 230
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-230

Query Match      100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 54
US-09-932-613-231
; Sequence 231, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 231
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-231

Query Match      100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 55
US-09-932-613-232
; Sequence 232, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 232
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-232

Query Match      100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 56
US-09-932-613-233
; Sequence 233, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
```

CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 233
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-233

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
DB 3 WYDPLTKLWL 12

RESULT 57
US-09-932-613-234
Sequence 234, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 234
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-234

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
DB 3 WYDPLTKLWL 12

RESULT 58
US-09-932-613-235
Sequence 235, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 235
LENGTH: 14
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-235

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
DB 3 WYDPLTKLWL 12

RESULT 59
US-09-932-613-236
Sequence 236, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 236
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-236

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
DB 3 WYDPLTKLWL 12

RESULT 60
US-09-932-613-237
Sequence 237, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 237
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-237

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
| | | | |
Db 3 WYDPLTKLML 12

RESULT 61
US-09-932-613-238

; Sequence 238, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-238

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
| | | | |
Db 3 WYDPLTKLML 12

RESULT 62

US-09-932-613-239
; Sequence 239, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 239
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-239

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
| | | | |
Db 3 WYDPLTKLML 12

RESULT 63
US-09-932-613-240

; Sequence 240, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-240

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
| | | | |
Db 3 WYDPLTKLML 12

RESULT 64
US-09-932-613-241

; Sequence 241, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-241

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
| | | | |
Db 3 WYDPLTKLML 12

RESULT 65
US-09-932-613-242

; Sequence 242, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.

```
/ APPLICANT: Potter, M. Daniel
/ APPLICANT: Fleming, Tony J.
/ APPLICANT: Rosen, Craig A.
/ TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
/ FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
/ CURRENT APPLICATION NUMBER: US/09/932,613
/ NUMBER OF SEQ ID NOS: 458
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 242
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-242

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 66
US-09-932-613-243
/ Sequence 243, Application US/09932613
/ Publication No. US20030091565A1
/ GENERAL INFORMATION:
/ APPLICANT: Human Genome Sciences, Inc.
/ APPLICANT: Beltzer, James P.
/ APPLICANT: Potter, M. Daniel
/ APPLICANT: Fleming, Tony J.
/ APPLICANT: Rosen, Craig A.
/ TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
/ FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
/ CURRENT APPLICATION NUMBER: US/09/932,613
/ NUMBER OF SEQ ID NOS: 458
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 243
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-243

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 67
US-09-932-613-244
/ Sequence 244, Application US/09932613
/ Publication No. US20030091565A1
/ GENERAL INFORMATION:
/ APPLICANT: Human Genome Sciences, Inc.
/ APPLICANT: Beltzer, James P.
/ APPLICANT: Potter, M. Daniel
/ APPLICANT: Fleming, Tony J.
/ APPLICANT: Rosen, Craig A.
/ TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
/ FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
/ CURRENT APPLICATION NUMBER: US/09/932,613
/ CURRENT FILING DATE: 2001-08-17
```

```
/ NUMBER OF SEQ ID NOS: 458
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 244
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-244

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 68
US-09-932-613-245
/ Sequence 245, Application US/09932613
/ Publication No. US20030091565A1
/ GENERAL INFORMATION:
/ APPLICANT: Human Genome Sciences, Inc.
/ APPLICANT: Beltzer, James P.
/ APPLICANT: Potter, M. Daniel
/ APPLICANT: Fleming, Tony J.
/ APPLICANT: Rosen, Craig A.
/ TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
/ FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
/ CURRENT APPLICATION NUMBER: US/09/932,613
/ NUMBER OF SEQ ID NOS: 458
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 245
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-245

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 69
US-09-932-613-246
/ Sequence 246, Application US/09932613
/ Publication No. US20030091565A1
/ GENERAL INFORMATION:
/ APPLICANT: Human Genome Sciences, Inc.
/ APPLICANT: Beltzer, James P.
/ APPLICANT: Potter, M. Daniel
/ APPLICANT: Fleming, Tony J.
/ APPLICANT: Rosen, Craig A.
/ TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
/ FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
/ CURRENT APPLICATION NUMBER: US/09/932,613
/ CURRENT FILING DATE: 2001-08-17
/ NUMBER OF SEQ ID NOS: 458
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 246
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
```


OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-246

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|||
DB 3 WYDPLTKLWL 12

RESULT 70

US-09-932-613-247
; Sequence 247, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 247
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-247

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|||
DB 3 WYDPLTKLWL 12

RESULT 71

US-09-932-613-248
; Sequence 248, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 248
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-248

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|||
DB 3 WYDPLTKLWL 12

RESULT 72
US-09-932-613-249
; Sequence 249, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 249
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-249

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|||
DB 3 WYDPLTKLWL 12

RESULT 73
US-09-932-613-250
; Sequence 250, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 250
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-250

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|||
DB 3 WYDPLTKLWL 12

RESULT 74
US-09-932-613-251

```

; Sequence 251, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 251
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-251

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
Db 3 WYDPLTKLWL 12

RESULT 75
US-09-932-613-252
; Sequence 252, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 252
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-252

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
Db 3 WYDPLTKLWL 12

RESULT 76
US-09-932-613-253
; Sequence 253, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
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; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 253
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-253

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
Db 3 WYDPLTKLWL 12

RESULT 77
US-09-932-613-254
; Sequence 254, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 254
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-254

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
Db 3 WYDPLTKLWL 12

RESULT 78
US-09-932-613-255
; Sequence 255, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
```

SEQ ID NO 255
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-255

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10
|||
Db 3 WYDPLTKLML 12

RESULT 79
US-09-932-613-256
Sequence 256, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Belzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 256
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-256

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10
|||
Db 3 WYDPLTKLML 12

RESULT 80
US-09-932-613-257
Sequence 257, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Belzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 257
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-257

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10
|||
Db 3 WYDPLTKLML 12

RESULT 81
US-09-932-613-258
Sequence 258, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Belzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 258
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-258

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10
|||
Db 3 WYDPLTKLML 12

RESULT 82
US-09-932-613-259
Sequence 259, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Belzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 259
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-259

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10
|||

Db 3 WYDPLTKLWL 12

RESULT 83
US-09-932-613-260
; Sequence 260, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 260
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-260

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
| | | | | | | | | |
Db 3 WYDPLTKLWL 12

RESULT 84
US-09-932-613-261
; Sequence 261, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 261
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-261

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
| | | | | | | | | |
Db 3 WYDPLTKLWL 12

RESULT 85
US-09-932-613-262
; Sequence 262, Application US/09932613
; Publication No. US20030091565A1

; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 262
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-262

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
| | | | | | | | | |
Db 3 WYDPLTKLWL 12

RESULT 86
US-09-932-613-263
; Sequence 263, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 263
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-263

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
| | | | | | | | | |
Db 3 WYDPLTKLWL 12

RESULT 87
US-09-932-613-264
; Sequence 264, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON

```
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 264
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
US-09-932-613-264

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
   |||||
   |||||
Db 3 WYDPLTKLML 12

RESULT 88
US-09-932-613-265
Sequence 265, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 265
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-265

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
   |||||
   |||||
Db 3 WYDPLTKLML 12

RESULT 89
US-09-932-613-266
Sequence 266, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 266
LENGTH: 14
```

```
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-266

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
   |||||
   |||||
Db 3 WYDPLTKLML 12

RESULT 90
US-09-932-613-267
Sequence 267, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 267
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-267

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
   |||||
   |||||
Db 3 WYDPLTKLML 12

RESULT 91
US-09-932-613-268
Sequence 268, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 268
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-268

Query Match          100.0%; Score 64; DB 10; Length 14;
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Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10
| | | | | | | |
Db 3 WYDPLTKLWL 12

RESULT 92

US-09-932-613-269
; Sequence 269, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 269
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-269

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10
| | | | | | | |
Db 3 WYDPLTKLWL 12

RESULT 93

US-09-932-613-270
; Sequence 270, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 270
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-270

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10
| | | | | | | |
Db 3 WYDPLTKLWL 12

RESULT 94
US-09-932-613-271
; Sequence 271, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 271
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-271

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10
| | | | | | | |
Db 3 WYDPLTKLWL 12

RESULT 95

US-09-932-613-272
; Sequence 272, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzter, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 272
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-272

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10
| | | | | | | |
Db 3 WYDPLTKLWL 12

RESULT 96

US-09-932-613-273
; Sequence 273, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.

```
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 273
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-273

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLML 10
        |||||
        3 WYDPLTKLML 12

RESULT 97
US-09-932-613-274
; Sequence 274, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 274
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-274

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLML 10
        |||||
        3 WYDPLTKLML 12

RESULT 98
US-09-932-613-275
; Sequence 275, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
```

```
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 275
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-275

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLML 10
        |||||
        3 WYDPLTKLML 12

RESULT 99
US-09-932-613-276
; Sequence 276, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 276
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-276

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLML 10
        |||||
        3 WYDPLTKLML 12

RESULT 100
US-09-932-613-277
; Sequence 277, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 277
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-277

Query Match 100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. NO. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|||
Db 3 WYDPLTKLWL 12

Search completed: July 12, 2004, 21:35:38
Job time : 47 secs

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OM protein - protein search, using sw model

Run on: July 12, 2004, 21:27:27 ; Search time 20 Seconds

(without alignments)
48.096 Million cell updates/sec

Title: US-09-932-613-457

Perfect score: 64

Sequence: 1 WYDPLTKML 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	71.9	870	1 GNMVUA	pol polypeptide -
2	45	70.3	383	2 B84608	hypothetical prote
3	45	70.3	482	2 G83928	hypothetical prote
4	43	67.2	567	2 AC0754	probable membrane
5	43	67.2	570	2 T20166	hypothetical prote
6	43	67.2	888	1 GNLJHD	pol polypeptide -
7	42	65.6	293	2 T05419	hypothetical prote
8	42	65.6	374	2 B85421	probable polypepti
9	42	65.6	374	2 T04672	polypeptide
10	42	65.6	392	2 T09371	hypothetical prote
11	41	64.1	655	2 F82138	GGBP family prote
12	41	64.1	672	2 H83315	hypothetical prote
13	40	62.5	202	2 S16442	MTP protein - mou
14	40	62.5	345	2 A45586	hypothetical prote
15	40	62.5	378	2 T47407	hypothetical prote
16	40	62.5	519	2 B87353	hypothetical prote
17	39	60.9	157	2 S49622	circ protein - Rho
18	39	60.9	158	2 A57438	tryptophan-rich se
19	39	60.9	176	1 F64725	probable NAD(P)H2
20	39	60.9	176	2 A85486	probable NAD(P)H o
21	39	60.9	176	2 A90635	probable NAD(P)H o
22	39	60.9	176	2 A10512	probable NAD(P)H o
23	39	60.9	308	1 MMLJSL	bel-1 protein - si
24	39	60.9	311	2 S18740	bell protein - sim
25	39	60.9	333	2 S42424	hypothetical prote
26	39	60.9	335	2 T46319	hypothetical prote
27	39	60.9	365	2 T08577	hypothetical prote
28	39	60.9	430	2 T20170	hypothetical prote
29	39	60.9	480	2 T20168	hypothetical prote

30	39	60.9	551	2 D71969	1-lactate permease
31	39	60.9	551	2 E64537	L-lactate permease
32	39	60.9	983	2 E86989	probable integral
33	39	60.9	2183	2 T37218	hypothetical prote
34	38	59.4	190	2 B83990	hypothetical prote
35	38	59.4	206	2 G69057	hypothetical prote
36	38	59.4	295	2 T32202	hypothetical prote
37	38	59.4	321	2 T50966	hypothetical prote
38	38	59.4	341	2 B83298	conserved hypotet
39	38	59.4	361	2 A13513	Arpase virB11 homo
40	38	59.4	380	2 T00683	hypothetical prote
41	38	59.4	491	2 AC2650	glucose-6-phosphat
42	38	59.4	503	2 B97432	L-lactate permease
43	38	59.4	549	2 D64537	L-lactate permease
44	38	59.4	560	2 F81423	L-lactate permease
45	38	59.4	803	2 F90485	hypothetical prote
46	38	59.4	849	2 T46253	hypothetical prote
47	38	59.4	888	2 T51593	GTP-binding regula
48	38	59.4	901	2 T01135	probable GTP-bind
49	38	59.4	1195	2 S76592	5-methyltetrahydro
50	38	59.4	1895	2 T15881	hypothetical prote
51	38	59.4	2825	2 T14271	DocA protein, stre
52	38	59.4	2825	2 T14271	hypothetical prote
53	37.5	58.6	227	2 A70865	conserved hypotet
54	37.5	58.6	227	2 B87102	conserved hypotet
55	37.5	58.6	301	1 C40626	dihydrodipicolinat
56	37	57.8	151	2 H87263	hypothetical prote
57	37	57.8	177	2 B85833	partial probable s
58	37	57.8	177	2 B90988	conserved hypotet
59	37	57.8	266	2 AB0665	conserved hypotet
60	37	57.8	315	2 B69751	hypothetical prote
61	37	57.8	316	2 T15395	hypothetical prote
62	37	57.8	349	2 S67858	guni protein - Xan
63	37	57.8	356	2 B82902	citrate-dependent
64	37	57.8	357	2 A95326	probable Altc [imp
65	37	57.8	363	1 BVBK2	MAK32 protein - Ye
66	37	57.8	383	1 S42003	sterol 24-C-methyl
67	37	57.8	384	2 T19377	conserved hypotet
68	37	57.8	388	2 AHI950	cardamoyl phosphat
69	37	57.8	401	2 B87503	acyl-CoA dehydroge
70	37	57.8	436	2 H87793	protein C27A12.8 [
71	37	57.8	606	2 A72429	oligopeptide ABC t
72	37	57.8	608	2 D72306	hypothetical prote
73	37	57.8	660	2 H13736	probable tpr prote
74	37	57.8	681	2 UX0338	rabphilin-3A - mou
75	37	57.8	704	2 I58166	rabphilin-3A - rat
76	37	57.8	784	2 A48097	rabphilin-3A - bov
77	37	57.8	819	2 A53714	protein kinase (EC
78	37	57.8	872	2 T37789	Scd1 protein - fis
79	37	57.8	965	2 T12545	hypothetical prote
80	37	57.8	985	1 DUBB11	DNA-directed DNA p
81	37	57.8	1105	2 B64973	yeag protein - Bsc
82	37	57.8	1337	2 T30291	dextranase - Strept
83	36.5	57.0	222	2 C75250	hypothetical prote
84	36.5	57.0	723	2 B87706	prolyl oligopeptid
85	36.5	57.0	867	2 S72842	methionine synthas
86	36.5	57.0	1206	2 B87072	hypothetical prote
87	36	56.2	209	2 AG1129	hypothetical prote
88	36	56.2	205	2 T16669	pregnancy-specific
89	36	56.2	312	2 T50960	related to nodulat
90	36	56.2	317	2 D64233	hypothetical prote
91	36	56.2	321	2 S59388	probable membrane
92	36	56.2	405	2 H82632	Arpase Xfr1828 [imp
93	36	56.2	418	2 T47818	hypothetical prote
94	36	56.2	419	2 S51715	hypothetical prote
95	36	56.2	424	2 F71488	hypothetical prote
96	36	56.2	427	2 A64945	probable membrane
97	36	56.2	427	2 C85795	hypothetical prote
98	36	56.2	427	2 G80946	probable membrane
99	36	56.2	428	2 QJ1864	hypothetical 47.0K
100	36	56.2	460	2 G82847	hypothetical prote
101	36	56.2	531	2 T33099	hypothetical prote
102	36	56.2	540	2 T20352	hypothetical prote

103	36	56.2	728	2	AB2405	hypothetical prote
104	36	56.2	808	1	T34557	hypothetical prote
105	36	56.2	863	1	GNHYIH	retrovirus-related
106	36	56.2	1148	2	S51855	hypothetical prote
107	36	56.2	1269	2	A90267	proteinase related
108	36	56.2	1276	2	S75801	probable phycho
109	36	56.2	1369	2	T43433	alpha-glucan synth
110	36	56.2	1872	2	T24683	hypothetical prote
111	35	54.7	55	2	E90620	ATP synthase F0 ch
112	35	54.7	103	2	E40899	hypothetical prote
113	35	54.7	115	2	A64496	hypothetical prote
114	35	54.7	140	2	B86683	hypothetical prote
115	35	54.7	140	2	C86800	prophage p13 prote
116	35	54.7	140	2	T46495	hypothetical prote
117	35	54.7	148	2	C90778	hypothetical prote
118	35	54.7	148	2	F91001	hypothetical prote
119	35	54.7	148	2	F85846	unknown protein en
120	35	54.7	148	2	H85639	hypothetical prote
121	35	54.7	188	2	F95935	probable glycosylt
122	35	54.7	191	2	B84207	probable acetyltra
123	35	54.7	203	2	E95280	conserved hypothet
124	35	54.7	254	2	AE2516	hypothetical prote
125	35	54.7	255	2	T03539	cobP protein - Rho
126	35	54.7	263	2	F45734	orf6 3' to hsd -
127	35	54.7	265	2	D87292	hypothetical prote
128	35	54.7	284	2	F84363	Birp-like homolog f
129	35	54.7	306	2	AC1835	hypothetical prote
130	35	54.7	316	2	T01637	gene R protein - A
131	35	54.7	329	2	H70744	hypothetical prote
132	35	54.7	341	2	S33464	hypothetical prote
133	35	54.7	342	2	A96581	hypothetical prote
134	35	54.7	350	1	JC4222	membrane dipeptida
135	35	54.7	353	2	C96573	protein p12M6.19
136	35	54.7	359	2	T16350	hypothetical prote
137	35	54.7	360	2	C85711	hypothetical prote
138	35	54.7	376	2	A72391	dihydrocoarlate - T
139	35	54.7	424	2	JC4057	probable C-14 ster
140	35	54.7	439	2	E98139	hypothetical prote
141	35	54.7	439	2	AF3148	hypothetical prote
142	35	54.7	465	2	C86911	probable cell-divi
143	35	54.7	465	2	T10012	probable cell divi
144	35	54.7	472	2	T43084	transfer complex p
145	35	54.7	478	2	F96594	unknown protein, 5
146	35	54.7	489	2	JC0767	beta-galactosidase
147	35	54.7	489	2	B90483	beta-galactosidase
148	35	54.7	491	2	AB3573	glucose-6-phosphat
149	35	54.7	497	2	G87793	protein C27A12.7 f
150	35	54.7	501	2	AS5090	aspartic proteinas
151	35	54.7	508	2	B81083	cardiolipin synthe
152	35	54.7	514	2	D89775	hypothetical prote
153	35	54.7	524	2	S73397	MG68 homolog R02
154	35	54.7	525	2	B81859	phospholipase D-fam
155	35	54.7	535	2	T04222	hypothetical prote
156	35	54.7	546	2	D86811	mannosyl-glycoprot
157	35	54.7	564	2	F90965	hypothetical prote
158	35	54.7	569	2	H64959	probable membrane
159	35	54.7	575	1	WFE0M	mullerian inhibiti
160	35	54.7	632	1	H83106	chemotactic transd
161	35	54.7	721	2	D83110	exodeoxyribonuclea
162	35	54.7	728	2	F97262	topoisomerase B f1
163	35	54.7	752	2	B82146	Rec2-related prote
164	35	54.7	801	2	A37353	membrane protein 4
165	35	54.7	822	2	S70012	methionine-S-oxide
166	35	54.7	843	2	T14579	translation elonga
167	35	54.7	867	1	GNLJSA	pol polypotein -
168	35	54.7	867	1	GNLJMP	pol polypotein (c
169	35	54.7	922	2	AG1827	maltooligosyltreha
170	35	54.7	1133	2	T12529	hypothetical prote
171	35	54.7	1215	2	T25078	hypothetical prote
172	35	54.7	1474	2	F69009	probable membrane
173	35	54.7	1476	2	AA5773	kelch protein, lon
174	35	54.7	1724	2	T13942	UNC-13-B protein -
175	35	54.7	1941	2	T30554	ubiquitin-protein
176	35	54.7	2207	2	T42759	Munc13-3 protein -
177	34.5	53.9	226	2	T35172	hypothetical prote
178	34.5	53.9	289	2	A11448	L-alanoyl-D-glutam
179	34.5	53.9	308	2	AC1645	N-acetylmutramoyl-L
180	34.5	53.9	316	2	AF1752	N-acetylmutramoyl-L
181	34.5	53.9	316	2	A11728	N-acetylmutramoyl-L
182	34.5	53.9	384	2	H81198	conserved hypothet
183	34.5	53.9	400	2	B81775	hypothetical intreg
184	34.5	53.9	412	2	S76239	hypothetical prote
185	34.5	53.9	423	2	H83603	hypothetical prote
186	34.5	53.9	449	2	F81954	ubiquinol-cytochro
187	34.5	53.9	449	2	E81011	ubiquinol-cytochro
188	34.5	53.1	115	2	AC1134	hypothetical prote
189	34	53.1	116	2	C64017	hypothetical prote
190	34	53.1	121	2	A12244	dihydroneopterin a
191	34	53.1	137	2	S50009	hypothetical prote
192	34	53.1	161	2	D39441	sporilGA homolog -
193	34	53.1	162	2	E87351	hypothetical prote
194	34	53.1	192	2	T35200	hypothetical prote
195	34	53.1	207	2	A70866	hypothetical prote
196	34	53.1	207	2	F87094	conserved hypothet
197	34	53.1	220	2	A86308	probable glutathio
198	34	53.1	224	2	A75170	ribonuclease hri f
199	34	53.1	227	2	A24911	prolactin-like pro
200	34	53.1	233	2	H90213	hypothetical prote
201	34	53.1	233	2	AB2491	transposase all710
202	34	53.1	233	2	AB2500	transposase all717
203	34	53.1	233	2	AC2571	transposase all856
204	34	53.1	233	2	AE2478	transposase all700
205	34	53.1	233	2	AG2515	transposase all730
206	34	53.1	233	2	AH2491	transposase all711
207	34	53.1	233	2	AH2524	transposase all737
208	34	53.1	253	2	C84544	probable ribonucle
209	34	53.1	261	2	T32562	hypothetical prote
210	34	53.1	262	2	A38116	hypothetical prote
211	34	53.1	290	2	G85040	probable xylogluca
212	34	53.1	292	2	A49539	xyloglucan endo-1,
213	34	53.1	293	2	B82508	GGDF family prote
214	34	53.1	309	2	A29812	sporulation protei
215	34	53.1	318	2	AC2442	hypothetical prote
216	34	53.1	327	2	T18766	hypothetical prote
217	34	53.1	331	2	T48867	dtDPglucose 4,6-de
218	34	53.1	361	2	AH2434	hypothetical prote
219	34	53.1	366	1	XNBYUG	UDPglucose-hexose-
220	34	53.1	368	2	T01597	hypothetical prote
221	34	53.1	370	1	XNPKUD	UDPglucose-hexose-
222	34	53.1	370	2	T49246	hypothetical prote
223	34	53.1	381	2	S08296	beta-lactamase (EC
224	34	53.1	381	2	S45109	beta-lactamase (EC
225	34	53.1	381	2	S39196	beta-lactamase (EC
226	34	53.1	387	1	S39643	acetate / acetoin
227	34	53.1	398	2	H86424	unknown protein f1
228	34	53.1	422	2	G70984	probable papas pro
229	34	53.1	423	2	S73020	hypothetical prote
230	34	53.1	435	2	C83903	hypothetical prote
231	34	53.1	435	2	E86266	protein F3F19.23 f
232	34	53.1	436	2	G97186	diverged glycosylt
233	34	53.1	439	2	AS9327	site-specific reco
234	34	53.1	448	2	T29040	hypothetical prote
235	34	53.1	470	2	A72494	hypothetical prote
236	34	53.1	472	2	D86828	glucuronate isomer
237	34	53.1	497	2	AC2518	transposase all732
238	34	53.1	497	2	AC2564	transposase all751
239	34	53.1	497	2	AD2511	transposase all726
240	34	53.1	505	2	T19871	hypothetical prote
241	34	53.1	506	2	T19973	hypothetical prote
242	34	53.1	518	2	S42387	permease fimported
243	34	53.1	521	2	D96992	catelase katC fimp
244	34	53.1	533	2	B83813	lysine-RNA ligase
245	34	53.1	533	2	T46875	hypothetical prote
246	34	53.1	534	2	C64367	WD repeat protein
247	34	53.1	543	2	T37570	catelase (EC 1.11.
248	34	53.1	547	2	E69647	

249 34 53.1 547 2 AG1813
250 34 53.1 551 2 D69282
251 34 53.1 551 2 A49904
252 34 53.1 551 2 A98189
253 34 53.1 551 2 B86036
254 34 53.1 551 2 AB0976
255 34 53.1 570 2 T24152
256 34 53.1 579 2 H88478
257 34 53.1 613 2 T36922
258 34 53.1 621 2 A42257
259 34 53.1 625 2 T25373
260 34 53.1 645 2 S49570
261 34 53.1 668 2 P81101
262 34 53.1 668 2 G81839
263 34 53.1 680 2 A81875
264 34 53.1 736 2 A86171
265 34 53.1 753 2 B96772
266 34 53.1 800 1 J50029
267 34 53.1 800 2 B59106
268 34 53.1 803 2 T10060
269 34 53.1 809 2 E71660
270 34 53.1 820 2 G82168
271 34 53.1 848 2 B86443
272 34 53.1 868 2 D69297
273 34 53.1 885 2 G91080
274 34 53.1 899 2 H85925
275 34 53.1 1044 2 H97186
276 34 53.1 1051 2 T43253
277 34 53.1 1097 2 G85092
278 34 53.1 1154 2 A39577
279 34 53.1 1178 2 A81845
280 34 53.1 1271 1 TYH08R
281 34 53.1 1578 2 S76238
282 34 53.1 1877 2 T40550
283 34 53.1 1731 1 VF1HJH
284 34 53.1 2733 2 S15760
285 34 53.1 5005 2 P82884
286 33.5 52.3 403 2 P83092
287 33.5 52.3 532 2 S73732
288 33.5 52.3 556 2 S39297
289 33.5 52.3 587 2 S39351
290 33.5 52.3 1529 2 A59189
291 33 51.6 98 2 T12887
292 33 51.6 99 2 S72162
293 33 51.6 103 2 A72134
294 33 51.6 141 2 T49659
295 33 51.6 158 2 B87271
296 33 51.6 182 2 S03445
297 33 51.6 183 2 A56579
298 33 51.6 201 2 A82235
299 33 51.6 202 2 S53980
300 33 51.6 203 2 S19714

ALIGNMENTS

RESULT 1

GNMVA
pol polyprotein - sheep pulmonary adenomatosis virus
N:Contains: endonuclease (EC 3.1.-.-): RNA-directed DNA polymerase (EC 2.7.7.49)
C:Species: sheep pulmonary adenomatosis virus
C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 08-Apr-1994
C/Accession: C42740
R:York, D.F.; Vigne, R.; Verwoerd, D.W.; Querat, G.
J. Virol. 66, 4930-4939, 1992
A:Title: Nucleotide sequence of the jaagsiekte retrovirus, an exogenous and endogenous
A:Reference number: A42740; MUID:9233675; PMID:1629959
A:Accession: C42740
A:Molecule type: genomic RNA
A:Residues: 1-870 <YOR>
A:Cross-references: GB:M60216
C:Comment: This protein is likely to be expressed as a gag-pol polyprotein.

C:Comment: The precise boundary between RNA-directed DNA polymerase and endonuclease has
C:Genetics:
A:Gene: pol
A:Start codon: UCA
C:Superfamily: pol polyprotein
C:Keywords: endonuclease; hydrolase; nucleotidyltransferase; polyprotein; reverse transcriptase

Query Match 71.9%; Score 46; DB 1; Length 870;
Best Local Similarity 77.8%; Pred. No. 6.5;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 WYDPLTKLM 9
Db 813 WKDPLTKLM 821

RESULT 2

B84608
hypothetical protein At2g22030 (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 14-Jul-2003
C/Accession: B84608
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nieman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: B84608
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <STO>
A:Cross-references: GB:AE02093; NID:94587593; PIDN:ADD25821.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g22030
A:Map position: 2
C:Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match 70.3%; Score 45; DB 2; Length 383;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 WYDPLTKLM 9
Db 288 WYDPLTKLM 296

RESULT 3

G83928
hypothetical protein BH2231 (imported) - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C/Accession: G83928
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Saeki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G83928
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-482 <STO>
A:Cross-references: GB:AP001514; GB:BA000004; NID:910174613; PIDN:BA05950.1; GSPDB:GN001
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2231

Query Match 70.3%; Score 45; DB 2; Length 482;
Best Local Similarity 77.8%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 WYDPLTKLM 9
Db 443 WYDPLTKLM 451

Db 91 WSDPISRMWI 100

RESULT 9

T04672

polygalacturonase homolog F8D20.180 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 03-Nov-2000

C:Accession: T04672

R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mewes,

submitted to the Protein Sequence Database, July 1998

A:Reference number: Z15381

A:Accession: T04672

A:Molecule type: DNA

A:Residues: 1-374 <BEV>

A:Cross-references: EMBL:AL031135

A:Experimental source: cultivar Columbia; BAC clone F8D20

C:Genetics:

A:Map position: 4

A>Note: intron positions not resolved

A>Note: F8D20.180

C:Superfamily: polygalacturonase

Query Match 65.6%; Score 42; DB 2; Length 374;
Best Local Similarity 40.0%; Pred. No. 13;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKML 10
|:|:|:|:
Db 91 WSDPISRMWI 100

RESULT 10

T09371

hypothetical protein F23K16.180 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 14-Jul-2003

C:Accession: T09371

R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, June 1999

A:Reference number: Z16552

A:Accession: T09371

A:Molecule type: DNA

A:Residues: 1-392 <BEV>

A:Cross-references: EMBL:AL078620; GSPDB:GN00062; ATSP:F23K16.180

A:Experimental source: cultivar Columbia; BAC clone F23K16

C:Genetics:

A:Gene: ATSP:F23K16.180

A:Map position: 4

C:Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match 65.6%; Score 42; DB 2; Length 392;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKML 9
|:|:|:|:
Db 297 WYDTMARLW 305

RESULT 11

F82138

GDEP family protein VC1934 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: F82138

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;

charlson, D.; Ermojaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellere, F

1, R.R.; Metalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen vibrio cholerae.

A:Reference number: A62035; MUID:20406833; PMID:10952301

A:Accession: F82138

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-655 <HEI>

A:Cross-references: GB:AE004269; GB:AE003852; NID:9656466; PIDN:AAF95082.1; GSPDB:GN001

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC1934

A:Map position: 1

Query Match 64.1%; Score 41; DB 2; Length 655;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKL 8
|:|:|:|:
Db 213 WHDPLTRL 220

RESULT 12

H83315

hypothetical protein PA2635 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: H83315

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; Lim,

Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho-

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: H83315

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-672 <STD>

A:Cross-references: GB:AE004692; GB:AE004091; NID:9948701; PIDN:AA06023.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA2635

C:Superfamily: Campylobacter jejuni hypothetical protein Cj0145

Query Match 64.1%; Score 41; DB 2; Length 672;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKML 10
|:|:|:|:
Db 566 WFDEPGRIMI 575

RESULT 13

S16442

MIP protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999

C:Accession: S16442; S16443; S19092

R:Chang-Yeh, A.; Mold, D.E.; Huang, R.C.C.

Nucleic Acids Res. 19, 3667-3672, 1991

A:Title: Identification of a novel murine IAD-promoted placenta-expressed gene.

A:Reference number: S16442; MUID:91305114; PMID:1906605

A:Accession: S16442

A:Molecule type: mRNA

A:Residues: 1-202 <CHA>

A:Cross-references: EMBL:X58523; NID:952733; PIDN:CAA41413.1; PID:952734

A>Note: the authors translated the codon GCT for residue 20 as Gln, TCA for residue 21 a-

A:Accession: S16443

A:Molecule type: DNA

A:Residues: 1-41 <CHA1>

A:Cross-references: EMBL:X58524

R:Chang-Yeh, A.

submitted to the EMBL Data Library, March 1991

A:Reference number: S19092

A:Accession: S19092

A:Molecule type: DNA

A:Residues: 1-25, 'AVDMRYVCATGQSM' <CH2>
A:Cross-references: EMBL:X58524; NID:g55733; PIDN:CAA414.1; PID:g55732
A>Note: the difference at the carboxyl end is due to a frameshift error

Query Match

Best Local Similarity 62.5%; Score 40; DB 2; Length 202;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 WYDPLTKLM 9
|||:|

Db 9 YDPTVKQW 16

RESULT 14

A43586
hypothetical protein 1 - Salmonella dublin plasmid PSD12

C:Species: Salmonella dublin

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-Oct-1999

C:Accession: A43586

R:Krause, M.; Harwood, J.; Fierer, J.; Guiney, D.

Infect. Immun. 59, 1860-1863, 1991

A:Title: Genetic analysis of homology between the virulence plasmids of Salmonella dublin

A:Reference number: A43586; MUID:91209947; PMID:1840573

A:Accession: A43586

A:Molecule type: DNA

A:Residues: 1-345 <KRA>

A:Cross-references: GB:M58505; NID:g154215; PIDN:AA27173.1; PID:g154216

C:Genetics:

A:Genome: plasmid

Query Match 62.5%; Score 40; DB 2; Length 345;
Best Local Similarity 50.0%; Pred. No. 27;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKML 10
|:|:|

Db 292 WLNPIERLWL 301

RESULT 15

T47407

hypothetical protein F23N14.90 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 14-Jul-2003

C:Accession: T47407

R:Blocker, H.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.; Quettler, F.; Salanoub

submitted to the Protein Sequence Database, March 2000

A:Reference number: Z24465

A:Accession: T47407

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-378 <BLO>

A:Cross-references: EMBL:AL138638

A:Experimental source: cultivar Columbia; BAC clone F23N14

C:Genetics:

A:Map position: 3

A>Note: F23N14.90

C:Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match 62.5%; Score 40; DB 2; Length 378;
Best Local Similarity 66.7%; Pred. No. 29;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
|||:|

Db 280 WYDSENKLM 288

RESULT 16

B87353
hypothetical protein CC0837 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: B87353

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Rmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: B87353

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-519 <STO>

A:Cross-references: GB:AE05673; NID:g13422090; PIDN:AAK2822.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC0837

Query Match 62.5%; Score 40; DB 2; Length 519;
Best Local Similarity 66.7%; Pred. No. 41;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
|||:|

Db 414 WYAPLAGLM 422

RESULT 17

S49622
crk protein - Rhodobacter sphaeroides

C:Species: Rhodobacter sphaeroides

C:Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 04-Sep-1998

C:Accession: S49622

R:Lang, H.P.; Cogdell, R.J.; Takachi, S.; Hunter, C.N.

submitted to the EMBL Data Library, November 1994

A:Description: The complete DNA sequence, specific TMS insertion map and gene assignment

A:Reference number: S49619

A:Accession: S49622

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-157 <LAN>

A:Cross-references: EMBL:X82458; NID:g575405; PID:g575409

C:Genetics:

A:Gene: crk

C:Superfamily: tryptophan-rich sensory protein

Query Match 60.9%; Score 39; DB 2; Length 157;
Best Local Similarity 66.7%; Pred. No. 17;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
|||:|

Db 30 WYDNLKFW 38

RESULT 18

A57438
tryptophan-rich sensory protein [similarity] - Rhodobacter sphaeroides (strain 2.4.1)

C:Species: Rhodobacter sphaeroides

C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 28-Jul-2000

C:Accession: A57438; T50747

R:Yeliseev, A.A.; Kaplan, S.

J. Biol. Chem. 270, 21167-21175, 1995

A:Title: A sensory transducer homologous to the mammalian peripheral-type benzodiazepine

A:Reference number: A57438; MUID:95403350; PMID:7673149

A:Accession: A57438

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-158 <YEL>

R:Choudhary, M.; Kaplan, S.

Nucleic Acids Res. 28, 862-867, 2000

A:Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2.

A:Reference number: Z25222; MUID:20115911; PMID:10648776

A:Accession: T50747

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <CHO>
A:Cross-references: EMBL:AF195122; PIDN:AAF24291.1
A:Experimental source: strain 2.4.1
C:Genetics:
A:Gene: tsps
C:Function:
A:Description: tsps negatively regulates the activity of coproporphyrinogen III oxidase
A>Note: tsps is supposed to cause the accumulation of a biosynthetic intermediate that is
C:Superfamily: tryptophan-rich sensory protein
C:Keywords: carotenoid biosynthesis

Query Match 60.9%; Score 39; DB 2; Length 158;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYD-PLTKML 9
DB 30 WYDNLNKPW 38

RESULT 19
F64725
probable NAD(P)H oxidoreductase (quinone) (EC 1.6.99.2) yabF - Escherichia coli (strain
C:Species: Escherichia coli
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C:Accession: F64725; S40567
R:Hayashi, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; PMID:97426617; PMID:9278503
A:Accession: F64725
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-176 <BLAT>
A:Cross-references: GB:AE000115; GB:U00096; NID:91786230; PIDN:AACT3157.1; PID:91786231;
A:Experimental source: strain K-12, substrain MG1655
R:Yuda, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Mizobu
submitted to the EMBL Data Library, December 1992
A:Description: Systematic sequencing of the Escherichia coli genome: analysis of the 0-2
A:Reference number: S40531
A:Accession: S40567
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-78, 'N', 80-122, 'G', 124-176 <YUR>
A:Cross-references: EMBL:D10483; NID:9216434; PIDN:BA01322.1; PID:9216471
C:Genetics:
A:Gene: yabF
C:Superfamily: NAD(P)H dehydrogenase (quinone) 2
C:Keywords: flavoprotein; NAD; oxidoreductase

Query Match 60.9%; Score 39; DB 1; Length 176;
Best Local Similarity 58.3%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD-PLTKML 10
DB 67 WYSIPPLKLM 78

RESULT 20
A85466
probable NAD(P)H oxidoreductase yabF [imported] - Escherichia coli (strain O157:H7, sub
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C:Accession: A85466
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glanier, J.D.; Rose, D.J.; Mayhew
iller, U.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dinalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; PMID:21074935; PMID:11206551
A:Accession: A85466

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-176 <STO>
A:Cross-references: GB:AE005174; NID:912512736; PIDN:AA654349.1; GSPDB:GN00145; UWGP:Z00
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yabF
C:Superfamily: NAD(P)H dehydrogenase (quinone) 2

Query Match 60.9%; Score 39; DB 2; Length 176;
Best Local Similarity 58.3%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD-PLTKML 10
DB 67 WYSIPPLKLM 78

RESULT 21
A90635
probable NAD(P)H oxidoreductase EC0049 [imported] - Escherichia coli (strain O157:H7, s
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C:Accession: A90635
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; PMID:21156231; PMID:11258796
A:Accession: A90635
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-176 <HAV>
A:Cross-references: GB:BA000007; PIDN:BA03472.1; PID:913359505; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 050952
C:Genetics:
A:Gene: EC0049
C:Superfamily: NAD(P)H dehydrogenase (quinone) 2

Query Match 60.9%; Score 39; DB 2; Length 176;
Best Local Similarity 58.3%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD-PLTKML 10
DB 67 WYSIPPLKLM 78

RESULT 22
A10512
probable NAD(P)H oxidoreductase STY0100 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typh
A>Note: this species has also been called Salmonella typh
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: A10512
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
.S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; PMID:21534947; PMID:11677608
A:Accession: A10512
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-176 <PAR>
A:Cross-references: GB:AL513382; PIDN:CA001241.1; PID:916501370; GSPDB:GN00176
C:Genetics:
A:Gene: STY0100
C:Superfamily: NAD(P)H dehydrogenase (quinone) 2

Query Match 60.9%; Score 39; DB 2; Length 176;
Best Local Similarity 58.3%; Pred. No. 20;

Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
QY 1 WYD--PLTKML 10
|||
Db 67 WYVPLTKMLW 78

RESULT 23

WMLJSL
bel-1 protein - simian foamy virus (type 1)

C:Species: simian foamy virus
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999
C:Accession: B39924
R:Merz, A.; Shaw, K.E.S.; Pratt-Lowe, E.; Barry, P.A.; Luciw, P.A.
J. Virol. 65, 2903-2909, 1991
A:Title: Identification of the simian foamy virus transcriptional transactivator gene (t
A:Reference number: A39924; MUID:91237804; PMID:1851862
A:Accession: B39924
A:Molecule type: DNA
A:Residues: 1-308 <MER>
A:Cross-references: GB:M74039; NID:G334878; PIDN:AAA47802.1; PID:G454845
C:Comment: This protein is a transcriptional transactivator.
C:Genetics:
A:Gene: bel-1; taf
C:Superfamily: foamy virus bel-1 protein
C:Keywords: transcription regulation

Query Match 60.9%; Score 39; DB 1; Length 308;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKML 10
|||
Db 155 YDPEELMW 163

RESULT 24

S18740
bell protein - simian foamy virus (fragment)

C:Species: simian foamy virus
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 31-Oct-1997
C:Accession: S18740
R:Kupiec, J.J.; Kay, A.; Hayat, M.; Ravier, R.; Perles, J.; Galibert, F.
Gene 101, 185-194, 1991
A:Title: Sequence analysis of the simian foamy virus type 1 genome.
A:Reference number: S18737; MUID:91276270; PMID:1647358
A:Accession: S18740
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-311 <KUP>
A:Cross-references: EMBL:X54482
C:Superfamily: foamy virus bel-1 protein

Query Match 60.9%; Score 39; DB 2; Length 311;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKML 10
|||
Db 158 YDPEELMW 166

RESULT 25

S42424
hypothetical protein y - Mycobacterium smegmatis

C:Species: Mycobacterium smegmatis
C:Date: 07-May-1998 #sequence_revision 15-May-1998 #text_change 22-Oct-1999
C:Accession: S42424; S31804
R:Cittillo, J.D.; Weisprod, T.R.; Pascopella, L.; Bloom, B.R.; Jacobs Jr., W.R.
Mol. Microbiol. 11, 629-639, 1994
A:Title: Isolation and characterization of the aspartokinase and aspartate semialdehyde
A:Reference number: S42421; MUID:94254720; PMID:7910936
A:Accession: S42424

A:Molecule type: DNA
A:Residues: 1-333 <CIR>
A:Cross-references: EMBL:Z17372; NID:G44506; PIDN:CA78987.1; PID:G581353
A:Note: the authors translated the initiation codon GTG for residue 1 as Val
C:Genetics:
A:Start codon: GTG

Query Match 60.9%; Score 39; DB 2; Length 333;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
|||
Db 209 WGDPAALM 217

RESULT 26

T48319
hypothetical protein F15A17.10 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2003
C:Accession: T48319
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysbaert, C.; Daseville, R.; De Clerck, R.; De
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24491
A:Accession: T48319
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-335 <BEV>
A:Cross-references: EMBL:AL163002
A:Experimental source: cultivar Columbia; BAC clone F15A17
C:Genetics:
A:Map position: 5
A:Note: F15A17.10
C:Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match 60.9%; Score 39; DB 2; Length 335;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKML 10
|||
Db 176 YDPTQTML 184

RESULT 27

T08577
hypothetical protein T22F8.190 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 14-Jul-2003
C:Accession: T08577
R:Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wandut, R.; Bancroft, I.; Mewes, H.W.; May
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16442
A:Accession: T08577
A:Molecule type: DNA
A:Residues: 1-365 <BEV>
A:Cross-references: EMBL:AL050351; GSPDB:GN00062; ATSP:T22F8.190
A:Experimental source: cultivar Columbia; BAC clone T22F8
C:Genetics:
A:Gene: ATSP:T22F8.190
A:Map position: 4
C:Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match 60.9%; Score 39; DB 2; Length 365;
Best Local Similarity 55.6%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
|||
Db 272 WYDSCKIM 280

RESULT 28

hypothetical protein C53A5.11 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T20170

R:Mortimore, B

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19232

A:Accession: T20170

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-430 <M11>

A:Cross-references: EMBL:Z81486; PIDN:CA030991.1; GSPDB:GN00023; CESP:C53A5.11

A:Experimental source: clone C53A5

C:Genetics:

A:Gene: CESP:C53A5.11

A:Map position: 5

A:Introns: 30/3; 52/3; 170/1; 240/3; 309/1

Query Match

Best Local Similarity 60.9%; Score 39; DB 2; Length 430;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9

DB 372 YDPLTKMT 379

RESULT 29

hypothetical protein C53A5.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T20168

R:Mortimore, B

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19232

A:Accession: T20168

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-480 <M11>

A:Cross-references: EMBL:Z81486; PIDN:CA030989.1; GSPDB:GN00023; CESP:C53A5.9

A:Experimental source: clone C53A5

C:Genetics:

A:Gene: CESP:C53A5.9

A:Map position: 5

A:Introns: 28/1; 59/3; 194/1; 264/3; 332/1

Query Match

Best Local Similarity 60.9%; Score 39; DB 2; Length 480;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9

DB 396 YDPLTKTW 403

RESULT 30

1-lactate permease - Helicobacter pylori (strain J99)

C:Species: Helicobacter pylori

A:Variety: strain J99

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 29-Sep-1999

C:Accession: D71969

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

Ives, C.; Gibson, R.; Werberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: D71969

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-551 <ARN>

A:Cross-references: GB:AE001452; GB:AE001439; NID:g4154639; PIDN:AA05719.1; PID:g415465

A:Experimental source: strain J99

C:Genetics:

A:Gene: lldp 2

C:Superfamily: L-lactate permease

Query Match

Best Local Similarity 60.9%; Score 39; DB 2; Length 551;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKML 10

DB 8 YDPLGNITWL 16

RESULT 31

1-lactate permease - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 29-Sep-1999

C:Accession: E64537

R:Tomb, J.F.; White, O.; Kervilave, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen-

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Frazer, C.;

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: E64537

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-551 <TOM>

A:Cross-references: GB:AE000535; GB:AE000511; NID:g2313217; PIDN:AA007209.1; PID:g231322

C:Genetics:

A:Start codon: GTG

C:Superfamily: L-lactate permease

Query Match

Best Local Similarity 60.9%; Score 39; DB 2; Length 551;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKML 10

DB 8 YDPLGNITWL 16

RESULT 32

Probable integral membrane protein [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: B66989

R:Coile, S.T.; Bigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho-

R.; Davies, R.M.; Devlin, K.; Dutchoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: B66989

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-983 <STD>

A:Cross-references: GB:AL450380; NID:G13092818; PIDN:CA030153.1; GSPDB:GN00147

C:Genetics:

A:Gene: ML0644

Query Match

Best Local Similarity 60.9%; Score 39; DB 2; Length 983;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YDPLTKLWL 10
|||:|:
A:Residues: 1-206 <MTH>
A:Cross-references: GB:AE000905; GB:AE000666; NID:g2622541; PIDN:AAH85908.1; PID:g2622541
A:Experimental source: strain Delta H
A:Gene: MTH1433

Db 666 YDPLTKVWM 674

RESULT 33
T37218
hypothetical protein SC2H4.02 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T37218
R:Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21615
A:Accession: T37218
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2183 <OLI>
A:Cross-references: EMBL:AL031514; PIDN:CAA20596.1; GSPDB:GN00070; SCOEDB:SC2H4.02
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC2H4.02

Query Match 60.9%; Score 39; DB 2; Length 2183;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLW 9
|||:|:
Db 1942 WTQPLTKWM 1950

RESULT 34
B83990
hypothetical protein BH2722 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: B83990
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: B83990
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-190 <STO>
A:Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAH06441.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2722

Query Match 59.4%; Score 38; DB 2; Length 190;
Best Local Similarity 70.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLW 10
|||:|:
Db 146 WTVDLTKLWL 155

RESULT 35
G69057
hypothetical protein MTH1433 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: G69057
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jivani, N.;
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funcit
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: G69057

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-206 <MTH>
A:Cross-references: GB:AE000905; GB:AE000666; NID:g2622541; PIDN:AAH85908.1; PID:g2622541
A:Experimental source: strain Delta H
A:Gene: MTH1433

Query Match 59.4%; Score 38; DB 2; Length 206;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLW 9
|||:|:
Db 106 YDPLTSRW 113

RESULT 36
T32202
hypothetical protein T02B11.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32202
R:Goela, D.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid T02B11.
A:Reference number: Z21135
A:Accession: T32202
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-295 <GOE>
A:Cross-references: EMBL:AF022979; PIDN:AAH69903.1; GSPDB:GN00023; CESP:T02B11.1
A:Experimental source: strain Bristol N2; clone T02B11
C:Genetics:
A:Gene: CESP:T02B11.1
A:Map position: 5
A:Introns: 161/3; 250/3

Query Match 59.4%; Score 38; DB 2; Length 295;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PLTKLWL 10
|||:|:
Db 3 PLTKLWL 9

RESULT 37
T50966
hypothetical protein B24P7.210 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C:Accession: T50966
R:Schulze, U.; Aign, V.; Hohnsbeil, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, July 2000
A:Reference number: Z25286
A:Accession: T50966
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-321 <SCH>
A:Cross-references: EMBL:AL389890; GSPDB:GN00116; NCSP:B24P7.210
A:Experimental source: BAC clone B24P7; strain OR74A
C:Genetics:
A:Gene: NCSP:B24P7.210
A:Map position: 6
A:Introns: 208/3

Query Match 59.4%; Score 38; DB 2; Length 321;
Best Local Similarity 55.6%; Pred. No. 55;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLW 9
|||:|:

DB 114 WYKTIATLM 122

RESULT 38

B83298

A:Description: hypothetical protein PA2771 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: B83298

A:Stature: C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,
L.; Lory, S.; Olson, M.V.

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: AB2950; MUID:2043737; PMID:10984043

A:Accession: B83298

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 <STO>

A:Cross-references: GB:AE004705; GB:AE004091; NID:g9948851; PIDN:AA06159.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA2771

Query Match 59.4%; Score 38; DB 2; Length 341;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 DPLTKLM 9
|||:|
Db 184 DPLTKLM 190

RESULT 39

A13513

A:Description: virB11 homolog BMEI10035 [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002

C:Accession: A13513

A:Stature: V.G.; Kapral, V.; Redkar, R.V.; Patra, G.; Mujer, C.; Ios, T.; Ivanova,
R.; Delvecchio, V.G.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Leves
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens

A:Reference number: AD3252; PMID:11756688

A:Accession: A13513

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-361 <KUR>

A:Cross-references: GB:AE008918; PIDN:AAU53276.1; PID:g17984158; GSPDB:GN00191

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEI10035

A:Map position: 11

C:Superfamily: tumor-inducing plasmid pTIC58 virB11 protein

Query Match 59.4%; Score 38; DB 2; Length 361;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WYDPLTK 7
|||:|
Db 343 WYDPLTK 349

RESULT 40

T00683

A:Description: protein At2g44030 [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein F6E13.16

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 14-Jul-2003

C:Accession: T00683; B84873

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, June 1998

A:Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.

A:Reference number: Z14180

A:Accession: T00683

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-380 <ROU>

A:Cross-references: EMBL:AC004005; NID:g3212846; PID:g3212860

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: AB4420; MUID:20083487; PMID:10617197

A:Accession: B84873

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-380 <STO>

A:Cross-references: GB:AE002093; NID:g3212860; PIDN:AA023411.1; GSPDB:GN00139

C:Genetics:

A:Gene: F6E13.16; At2g44030

A:Map position: 2

C:Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match 59.4%; Score 38; DB 2; Length 380;
Best Local Similarity 62.5%; Pred. No. 66;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 YDPLTKLM 9
|||:|
Db 192 YDPLTKLM 199

RESULT 41

AC2650

A:Description: glucose-6-phosphate 1-dehydrogenase zwf [imported] - Agrobacterium tumefaciens (strain C

C:Species: Agrobacterium tumefaciens

C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

C:Accession: AC2650

A:Stature: D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, P.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCella
; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F
ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AC2650

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-491 <KUR>

A:Cross-references: GB:AE006688; PIDN:AAU41617.1; PID:g17738955; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: zwf

A:Map position: circular chromosome

C:Superfamily: glucose-6-phosphate dehydrogenase

Query Match 59.4%; Score 38; DB 2; Length 491;
Best Local Similarity 55.6%; Pred. No. 86;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9
|||:|
Db 448 WYDPLTKLM 456

RESULT 42

B97432

A:Description: glucose-6-phosphate 1-dehydrogenase (6p6d) [imported] - Agrobacterium tumefaciens (strain

C:Species: Agrobacterium tumefaciens

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002

C:Accession: B97432

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Mollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
 A;Reference number: A97459; MUID:21608551; PMID:11743194
 A;Accession: B97432
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-503 <KUR>
 A;Cross-references: GB:AE007869; PIDN:AAK86411.1; PID:g15155545; GSPDB:GN00169
 C;Genetics:
 A;Gene: AGR_C_1065
 A;Map position: circular chromosome
 C;Superfamily: glucose-6-phosphate dehydrogenase

Query Match 59.4%; Score 38; DB 2; Length 503;
 Best Local Similarity 55.6%; Pred. No. 88;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
 |||: |||
 Db 460 WIDPLKSW 468

RESULT 43
 C71969
 L-lactate permease - *Helicobacter pylori* (strain J99)
 C;Species: *Helicobacter pylori*
 A;Variety: strain J99
 C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 29-Sep-1999
 C;Accession: C71969
 R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Miller, S.D.; Jiang, Q.; Taylor, D.E.; Voris, G.F.; Nature 397, 176-180, 1999
 A>Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
 A;Reference number: A71800; MUID:99120557; PMID:9923682
 A;Accession: C71969
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-549 <ARN>
 A;Cross-references: GB:AE001452; GB:AE001439; NID:g4154639; PIDN:AAD05718.1; PID:g415464
 A;Experimental source: strain J99
 C;Genetics:
 A;Gene: lldp_1
 C;Superfamily: L-lactate permease

Query Match 59.4%; Score 38; DB 2; Length 549;
 Best Local Similarity 66.7%; Pred. No. 96;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLW 10
 |||: |||
 Db 7 YDPLGH1WL 15

RESULT 44
 D64537
 L-lactate permease - *Helicobacter pylori* (strain 26695)
 C;Species: *Helicobacter pylori*
 C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 29-Sep-1999
 C;Accession: D64537
 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khatik, H.G.; Glodek, A.; McKenney, Nature 388, 539-547, 1997
 A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
 A;Reference number: A64520; MUID:97394467; PMID:9252185
 A;Accession: D64537
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-549 <TOM>
 A;Cross-references: GB:AE000535; GB:AE000511; NID:g2313217; PIDN:AAD07208.1; PID:g231322

C;Superfamily: L-lactate permease

Query Match 59.4%; Score 38; DB 2; Length 549;
 Best Local Similarity 66.7%; Pred. No. 96;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLW 10
 |||: |||
 Db 7 YDPLGH1WL 15

RESULT 45
 F81423
 L-lactate permease Cj0076c [imported] - *Campylobacter jejuni* (strain NCTC 11168)
 C;Species: *Campylobacter jejuni*
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
 C;Accession: F81423
 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling Nature 403, 665-668, 2000
 A>Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp
 A;Reference number: A81250; MUID:20150912; PMID:10688204
 A;Accession: F81423
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-560 <PAR>
 A;Cross-references: GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAW72562.1; PID:g696757;
 A;Experimental source: serotype O2, strain NCTC 11168
 C;Genetics:
 A;Gene: lcp; Cj0076c
 C;Superfamily: L-lactate permease

Query Match 59.4%; Score 38; DB 2; Length 560;
 Best Local Similarity 55.6%; Pred. No. 98;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLW 10
 |||: |||
 Db 11 YDPLSN1WL 19

RESULT 46
 F90485
 hypothetical protein SSO3039 [imported] - *Sulfolobus solfataricus*
 C;Species: *Sulfolobus solfataricus*
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 21-Jul-2003
 C;Accession: F90485
 R;Sne, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-t Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. Nature 403, 665-668, 2000
 A;Title: The complete genome sequence of the hyperthermophilic archaeon *Sulfolobus solfataricus* submitted to Genbank, April 2001
 A;Description: *Sulfolobus solfataricus* complete genome.
 A;Reference number: A99139
 A;Accession: F90485
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-803 <KUR>
 A;Cross-references: GB:AE006641; NID:g13816440; PIDN:AAK43141.1; GSPDB:GN00155
 C;Genetics:
 A;Gene: SSO3039
 C;Superfamily: beta-glucosidase, GBA2 type

Query Match 59.4%; Score 38; DB 2; Length 803;
 Best Local Similarity 62.5%; Pred. No. 1.4e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 8
 |||: |||
 Db 596 WYDPLSNL 603

RESULT 47
 T46253

hypothetical protein DKFZp761F171.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T46253
R:Ostenwelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: 223031
A:Accession: T46253
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-849 <AAA>
A:Cross-references: EMBL:AL137500
A:Experimental source: adult amygdala; clone DKFZp761F171
C:Genetics:
A:Note: DKFZp761F171.1

Query Match 59.4%; Score 38; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 1.56+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDPLTKL 8
|||
Db 491 YDPLTKL 497

RESULT 48
T51593
GTP-binding regulatory protein extra-large [validated] - Arabidopsis thaliana
N:Alternate names: G-protein extra-large
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: T51593
R:Lee, Y.R.; Asmann, S.M.
Plant Mol. Biol. 40, 55-64, 1999
A:Title: Arabidopsis thaliana 'extra-large GTP-binding protein' (AtXUG1): a new class of
A:Reference number: 225403; MUID:99320868; PMID:10394945
A:Accession: T51593
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-888 <LEE>
A:Cross-references: EMBL:AF060941; PIDN:AAC19352.1
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: XUG1
C:Function:
A:Description: binds GTP with specificity [validated, MUID:99320868]

Query Match 59.4%; Score 38; DB 2; Length 888;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
|||
Db 348 WYDPLTKLW 356

RESULT 49
T01135
probable GTP-binding protein (extra large) [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F26B6.11
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 02-Feb-2001
C:Accession: T01135; A84625
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.
A:Reference number: 214198
A:Accession: T01135
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-901 <ROU>
A:Cross-references: EMBL:AC003040; NID:G3242700; PID:G3242700
A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Unayama, L.; Tallon, L.
eius, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84625
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-901 <STO>
A:Cross-references: GB:AE02093; NID:G3242709; PIDN:AAC3761.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g23460; F26B6.11
A:Map position: 2
A:Introns: 358/3; 439/3; 502/3; 565/1; 646/3; 701/2

Query Match 59.4%; Score 38; DB 2; Length 901;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
|||
Db 348 WYDPLTKLW 356

RESULT 50
S76592
5-methyltetrahydrofolate-homocysteine S-methyltransferase (EC 2.1.1.13) [similarity] - S.
A:Species: Synchocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 03-Jun-2002
C:Accession: S76592
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis
S.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76592
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1195 <KAN>
A:Cross-references: EMBL:D64002; GB:AB001339; NID:G1001612; PIDN:BAAL0438.1; PID:G1001701
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: cobalamin-dependent methionine synthase; cobalamin-binding homology
F:Keywords: methyltransferase
F:737/Binding site: methylcobalamin cobalt (His) (axial ligand) #status predicted

Query Match 59.4%; Score 38; DB 2; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDPLTKL 8
|||
Db 611 YDPLTKL 617

RESULT 51
T15881
hypothetical protein D1044.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15881
R:Pauley, A.
submitted to the EMBL Data Library, June 1994
A:Description: The sequence of C. elegans cosmid D1044.
A:Reference number: 218423
A:Accession: T15881
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1895 <PAU>
A:Cross-references: EMBL:U00065; NID:G495681; PID:G495684; PIDN:AAA50735.1; CESP:D1044.3
A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:DL044.3
A:Query: 35/2; 63/2; 150/1; 191/3; 207/2; 405/3; 551/3; 629/1; 764/1; 933/1; 959/2; 10

Query Match
Best Local Similarity 59.4%; Score 38; DB 2; Length 1895;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKML 9
||| |||
Db 659 YDPLTKML 666

RESULT 52

T14271

Doc4 protein, stress-induced - mouse
N:Alternate names: odz protein homolog
C:Species: Mus musculus (house mouse)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14271

R:Wang, X.Z.; Kuroda, M.; Sok, J.; Batchvarova, N.; Kimmel, R.; Chung, P.; Zinszner, H.;
EMBO J. 17, 3613-3630, 1998

A:Title: Identification of novel stress-induced genes downstream of chop.
A:Reference number: 217951; PMID:98315054; PMID:9649432

A:Accession: T14271
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-2825 <MAN>
A:Cross-references: EMBL:AF059485; NID:g3170614; PID:g3170615; PIDN:AAC31807.1

C:Genetics:
A:Gene: Doc4

Query Match
Best Local Similarity 59.4%; Score 38; DB 2; Length 2825;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDPLTKML 8
||| |||
Db 2463 YDPLTKML 2469

RESULT 53

A70885
Hypothetical protein RV2794c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: A70885
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; PMID:98295987; PMID:9634230

A:Accession: A70885
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Residues: 1-227 <CO>
A:Molecule type: DNA

A:Cross-references: GB:AL00967; GB:AL123456; NID:g3261491; PIDN:CAA15589.1; PID:g262431

A:Experimental source: strain H37RV
C:Genetics:

A:Gene: RV2794c
Query Match
Best Local Similarity 58.6%; Score 37.5; DB 2; Length 227;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 WYDPLTKML 10
||| |||
Db 163 WF-PLTKML 171

RESULT 54

E87102

Conserved hypothetical protein ML1547 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: E87102
R:Cole, S.T.; Sigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
S.; M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; PMID:21128732; PMID:11234002

A:Accession: E87102
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-227 <STO>

A:Cross-references: GB:AL450380; NID:g13093366; PIDN:CAC30498.1; GSPDB:GN00147

C:Genetics:
A:Gene: ML1547

Query Match
Best Local Similarity 58.6%; Score 37.5; DB 2; Length 227;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 WYDPLTKML 10
||| |||
Db 163 WF-PLTKML 171

RESULT 55

C40626
dihydrodipicolinate synthase (EC 4.2.1.52) precursor [similarity] - Corynebacterium glut

N:Alternate names: L-2,3-dihydrodipicolinate synthetase
C:Species: Corynebacterium glutamicum
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 17-Mar-2000

C:Accession: C40626; S12105
R:Pisabarro, A.; Malumbres, M.; Mateos, I.M.; Oguita, J.A.; Martin, J.F.
J. Bacteriol. 175, 2743-2749, 1993

A:Title: A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum
ion.

A:Reference number: A40626; PMID:93239702; PMID:8478336

A:Accession: C40626
A:Molecule type: DNA

A:Residues: 1-301 <PIS>
A:Cross-references: GB:Z21502; GB:S59668; NID:g311767; PIDN:CAA79714.1; PID:g311770

A:Experimental source: ATCC 13639
A>Note: Sequence extracted from NCBI backbone (NCBIN:130448, NCBIP:130451)

R:Bommasalle, S.; Oreglia, J.; Sicard, A.M.
Nucleic Acids Res. 18, 6421, 1990

A:Title: Nucleotide sequence of the dapA gene from Corynebacterium glutamicum.
A:Reference number: S12105; PMID:91057127; PMID:2129555

A:Accession: S12105
A:Molecule type: DNA

A:Residues: 1-265, 'S', 267-301 <BON>
A:Cross-references: EMBL:X53993; NID:g40490; PIDN:CAA37940.1; PID:g40491

A:Experimental source: AS019
C:Genetics:

A:Gene: dapA
A:Function:

A:Description: catalyzes the condensation of pyruvate and L-aspartate 4-semialdehyde to L
A:Pathway: diaminopimelate-lysine biosynthesis
A>Note: this enzyme may catalyze only the condensation of pyruvate and L-aspartate 4-sem

C:Superfamily: dihydrodipicolinate synthase
C:Keywords: carbon-oxygen lyase; diaminopimelate-lysine biosynthesis; hydro-lyase

F:173/Active site: Lys (covalent pyruvate-binding) #status Predicted

Query Match
Best Local Similarity 58.6%; Score 37.5; DB 1; Length 301;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 WY--DPLTKML 10
||| |||

Db 193 WYSGDDPLNLAWML 205

RESULT 56
H87263
hypothetical protein CC0121 [imported] - *Caulobacter crescentus*
C:Species: *Caulobacter crescentus*
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: H87263
R:Niemann, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laid, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Esmolaev, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87263
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151 <STO>
A:Cross-references: GB:AE005673; NID:g13421228; PIDN:AK22108.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC0121

Query Match 57.8%; Score 37; DB 2; Length 151;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
| | | | |
| | | | |
Db 37 WRDPVREAWL 46

RESULT 57
B85833
partial probable sensor kinase Z3235 [imported] - *Escherichia coli* (strain O157:H7, sub
C:Species: *Escherichia coli*
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: B85833
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Hiller, L.; Grobeck, B.J.; Davis, N.W.; Lam, A.; Diallatia, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: B85833
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-177 <STO>
A:Cross-references: GB:AE005174; NID:g12516269; PIDN:AG57129.1; GSPDB:GN00145; UWGP:Z32
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z3235

Query Match 57.8%; Score 37; DB 2; Length 177;
Best Local Similarity 58.3%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYDPLTKLWL 10
| | | | |
| | | | |
Db 114 WYNPLQNLADWL 125

RESULT 58
B90988
partial probable sensor kinase ECS2874 [similarity] - *Escherichia coli* (strain O157:H7,
C:Species: *Escherichia coli*
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
C:Accession: B90988
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasanara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: B90988

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-177 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA836297.1; PID:g13362343; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECS2874

Query Match 57.8%; Score 37; DB 2; Length 177;
Best Local Similarity 58.3%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYDPLTKLWL 10
| | | | |
| | | | |
Db 114 WYNPLQNLADWL 125

RESULT 59
AB0665
conserved hypothetical protein STY1429 [imported] - *Salmonella enterica* subsp. *enterica*
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh
A>Note: this species has also been called *Salmonella typh*
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AB0665
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Comerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
Nature 413, 848-852, 2001
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AB0665
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD01691.1; PID:g16502542; GSPDB:GN00176
C:Genetics:
A:Gene: STY1429

Query Match 57.8%; Score 37; DB 2; Length 266;
Best Local Similarity 50.0%; Pred. No. 67;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
| | | | |
| | | | |
Db 110 WHIPAKIKWL 119

RESULT 60
B69751
conserved hypothetical protein ybgG - *Bacillus subtilis*
C:Species: *Bacillus subtilis*
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: B69751
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; BERTER
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Erttington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinis
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y.M.; Ogawa, K.; Ogatawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetalle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Seror
akeuchi, M.; Takamashi, A.; Tanaka, T.; Terpetre, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winers, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: B69751
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A;Residues: 1-315 <KUN>
A;Cross-references: GB:Z99105; GB:AL009126; NID:g262457; PIDN:CAB12035.1; PID:e1182193
A;Experimental source: strain 168
C;Genetics:
A;Gene: ybgg

submitted to the Protein Sequence Database, March 1992
A:Reference number: S19429
A:Accession: S19429
A:Molecule type: DNA
A:Residues: 1-363 <FEU>
A:Cross-references: EMBL:X59720; NID:g1907116; PIDN:CAA42310.1; PID:g1907162; GSPDB:GN001
R:Toh-e, A.; Sabaishi, Y.
Yeast 1, 159-171, 1985
A:Title: The PET10 locus of *Saccharomyces cerevisiae*: a complex locus containing multiple
A:Reference number: S07692; MUID:89131254; PMID:3916862
A:Accession: S07695
A:Molecule type: DNA
A:Residues: 1-14, '1', 15-81, 83-282, 'S', 284-363 <TOH>
C:Genetics:
A:Gene: SGD:MAK32; MIPS:YCR019W
A:Cross-references: SGD:S0000612; MIPS:YCR019W
A:Map position: 3R
C:Superfamily: MAK32 protein

Query Match 57.8%; Score 37; DB 1; Length 363;
Best Local Similarity 62.5%; Pred. No. 93;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLW 9
DB 325 YDPLTKW 332

RESULT 66
S42003
sterol 24-C-methyltransferase (EC 2.1.1.41) - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: PDR4-region bioc homolog; protein YM571.10c; protein YML008c
C:Species: *Saccharomyces cerevisiae*
C:Date: 03-Feb-1994 #sequence_revision 27-Jan-1995 #text_change 03-Jun-2002
C:Accession: S42003; PB0402; S55111; S17001; S35982
R:Hardwick, K.G.; Pelham, H.R.B.
Yeast 10, 265-269, 1994
A:Title: SPM6 is identical to ERG6, and encodes a putative methyltransferase required for
A:Reference number: S42003; MUID:94262330; PMID:8203167
A:Accession: S42003
A:Molecule type: DNA
A:Residues: 1-383 <HAR>
A:Cross-references: EMBL:X74249; NID:9396514; PIDN:CAA5308.1; PID:9396515
A:Note: the authors translated the codon ACT for residue 322 as Ala
R:Hussain, M.; Lenard, J.
Gene 101, 149-152, 1991
A:Title: Characterization of PDR4, a *Saccharomyces cerevisiae* gene that confers pleiotropic
A:Reference number: JB0416; MUID:91285426; PMID:2060792
A:Accession: PB0402
A:Molecule type: DNA
A:Residues: 1-258 <HUS>
A:Cross-references: GB:X53830; NID:94121; PIDN:CAA37826.1; PID:94122
A:Note: the authors suggested that this protein is unrelated to the pleiotropic drug res
nown to be a transcriptional activator (see PIR:S16706)
R:Gentles, S.; Bowman, S.
submitted to the EMBL Data Library, June 1995
A:Reference number: S55102
A:Accession: S55111
A:Molecule type: DNA
A:Residues: 1-383 <GEN>
A:Cross-references: EMBL:Z49810; NID:9854472; PIDN:CAA89944.1; PID:9854482; GSPDB:GN0001
C:Experimental source: strain AB972
C:Genetics:
A:Gene: SGD:ERG6; SED6; MIPS:YML008C
A:Cross-references: SGD:S0004467; MIPS:YML008C
A:Map position: 13L
C:Superfamily: 24-sterol C-methyltransferase; bioc homolog
C:Keywords: methyltransferase; S-adenosylmethionine
F:120-224/Domain: bioc homolog <BIOC>

Query Match 57.8%; Score 37; DB 1; Length 383;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
DB 286 WYDPLTKW 294

RESULT 67
T39377
conserved hypothetical protein SPBC12C2.04 - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C:Accession: T39377
R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, September 1995
A:Reference number: Z21849
A:Accession: T39377
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-384 <DEV>
A:Cross-references: EMBL:Z54140; PIDN:CAA90817.1; GSPDB:GN00066; SPDB:SPBC12C2.04
A:Experimental source: strain 972h-; cosmid c12C2
C:Genetics:
A:Gene: SPDB:SPBC12C2.04
C:Superfamily: *Schizosaccharomyces pombe* hypothetical protein SPAC2B1.17

Query Match 57.8%; Score 37; DB 2; Length 384;
Best Local Similarity 75.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 8
DB 247 WYDPLTKLW 254

RESULT 68
AH1950
carbamoyl phosphate synthase small chain [imported] - *Nostoc* sp. (strain PCC 7120)
C:Species: *Nostoc* sp. PCC 7120
A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AH1950
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasanuma, S.; Matsuda, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tanaka, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH1950
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-388 <KAN>
A:Cross-references: GB:BA000019; PIDN:BA073112.1; PID:917130501; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr1155
C:Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain; carbamo

Query Match 57.8%; Score 37; DB 2; Length 388;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
DB 173 WSDPTTAVW 181

RESULT 69
BB7503
acyl-CoA dehydrogenase family protein [imported] - *Caulobacter crescentus*
C:Species: *Caulobacter crescentus*
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 03-Aug-2001
C:Accession: BB7503
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kjolton, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A>Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A/Reference number: A87249; MUID:21173698; PMID:11259647
 A/Accession: B87503
 A>Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-401 <STO>
 A/Cross-references: GB:AE005673; NID:g13423526; PIDN:AAK24022.1; GSPDB:GN00148
 C/Genetics:
 A/Gene: CC2049
 C/Superfamily: acyl-CoA dehydrogenase

Query Match 57.8%; Score 37; DB 2; Length 401;
 Best Local Similarity 60.0%; Pred. No. 1e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 ||:|||||
 Db 46 WKRPDAKWL 55

RESULT 70
 H87793
 protein C27A12.8 [imported] - *Caenorhabditis elegans*
 C/Species: *Caenorhabditis elegans*
 C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C/Accession: H87793
 R/Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A>Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
 A/Reference number: A75000; MUID:99069613; PMID:9851916
 A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_eleg
 A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A/Accession: H87793
 A>Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-436 <STO>
 A/Cross-references: GB:chr_1; PIDN:AA93645.1; PID:g2105480; GSPDB:GN00019; CESP:C27A12.
 C/Genetics:
 A/Gene: C27A12.8
 A/Map position: 1

Query Match 57.8%; Score 37; DB 2; Length 436;
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 1 WYDP---LTKLWL 10
 ||:|||||
 Db 220 WHEPVCRLKWL 233

RESULT 71
 A72429
 oligopeptide ABC transporter, periplasmic oligopeptide-binding protein - *Thermotoga maritima*
 C/Species: *Thermotoga maritima*
 C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C/Accession: A72429
 R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
 Nature 399, 323-329, 1999
 A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A/Reference number: A72200; MUID:99287316; PMID:10360571
 A/Accession: A72429
 A>Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-606 <ARN>
 A/Cross-references: GB:AE001690; GB:AE000512; NID:g4980496; PIDN:AAD35125.1; PID:g498051
 A/Experimental source: strain MSB8
 C/Genetics:
 A/Gene: TM0031

C/Superfamily: dipeptide transport protein

Query Match 57.8%; Score 37; DB 2; Length 606;
 Best Local Similarity 50.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 ||:|||||
 Db 533 WYESTKXYI 542

RESULT 72
 D72306
 hypothetical protein - *Thermotoga maritima* (strain MSB8)
 C/Species: *Thermotoga maritima*
 C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 28-Jul-2000
 C/Accession: D72306
 R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
 Nature 399, 323-329, 1999
 A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A/Reference number: A72200; MUID:99287316; PMID:10360571
 A/Accession: D72306
 A>Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-608 <ARN>
 A/Cross-references: GB:AE001763; GB:AE000512; NID:g4981551; PIDN:AAD36097.1; PID:g498156
 A/Experimental source: strain MSB8
 C/Genetics:
 A/Gene: TM1020
 C/Superfamily: *Thermotoga maritima* hypothetical protein TM1020

Query Match 57.8%; Score 37; DB 2; Length 608;
 Best Local Similarity 60.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 ||:|||||
 Db 201 WYETKLYL 210

RESULT 73
 H71376
 probable tpr protein B (tprB) - *Syphilis spirochete*
 C/Species: *Treponema pallidum* subsp. *pallidum* (*Syphilis spirochete*)
 C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
 C/Accession: H71376
 R/Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McDor, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A>Title: Complete genome sequence of *Treponema pallidum*, the *Syphilis spirochete*.
 A/Reference number: A71250; MUID:98332770; PMID:9665876
 A/Accession: H71376
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-660 <COL>
 A/Cross-references: GB:AE001186; GB:AE000520; NID:g3322263; PIDN:AA65006.1; PID:g332226
 A/Experimental source: strain Nichols
 C/Genetics:
 A/Gene: TP0011
 C/Superfamily: *Treponema pallidum* tprL protein

Query Match 57.8%; Score 37; DB 2; Length 660;
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKL 8
 ||:||||
 Db 485 WYDSLTKL 492

RESULT 74

JX0338

rabphilin-3A - mouse

N.Alternate names: Rab3A, a ras p21 related small GTP binding protein

C.Species: Mus musculus (house mouse)

C.Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 07-May-1999

C.Accession: JX0338

R.Inagaki, N.; Mizuta, M.; Seino, S.

J.Biochem. 116, 239-242, 1994

A.Title: Cloning of a mouse rabphilin-3A expressed in hormone-secreting cells.

A.Reference number: JX0338; MUID:95122445; PMID:782236

A.Accession: JX0338

A.Molecule type: mRNA

A.Residues: 1-681 <INA>

A.Cross-references: DDBJ:D29965

C.Superfamily: protein kinase C C2 region homology

F.J37-489/Domain: protein kinase C C2 region homology <KC2A>

F.J531-646/Domain: protein kinase C C2 region homology <KC2B>

Query Match

Best Local Similarity 57.8%; Score 37; DB 2; Length 681;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DPLTKLWL 10

Db 574 DPFVKLWL 581

RESULT 75

I58166

rabphilin-3A - rat

C.Species: Rattus norvegicus (Norway rat)

C.Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999

C.Accession: I58166

R.Li, C.; Takei, K.; Geppert, M.; Daniell, L.; Stenius, K.; Chapman, E.R.; Jahn, R.; De

Neuron 13, 885-898, 1994

A.Title: Synaptic targeting of rabphilin-3A, a synaptic vesicle Ca2+/phospholipid-binding

A.Reference number: I58166; MUID:95033210; PMID:7946335

A.Accession: I58166

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Molecule type: mRNA

A.Residues: 1-684 <RES>

A.Cross-references: EMBL:U12571; NID:9533710; PIDN:AAA62662.1; PID:9533711

C.Superfamily: protein kinase C C2 region homology

F.J37-492/Domain: protein kinase C C2 region homology <KC2A>

F.J534-649/Domain: protein kinase C C2 region homology <KC2B>

Query Match

Best Local Similarity 75.0%; Score 37; DB 2; Length 684;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DPLTKLWL 10

Db 577 DPFVKLWL 584

RESULT 76

A48097

rabphilin-3A - bovine

C.Species: Bos primigenius taurus (cattle)

C.Date: 21-Jan-1999 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C.Accession: A48097

R.Shirataki, H.; Kaibuchi, K.; Sakoda, T.; Kishida, S.; Yamaguchi, T.; Wada, K.; Miyazaki

Mol. Cell. Biol. 13, 2061-2068, 1993

A.Title: Rabphilin-3A, a putative target protein for smg p25A/rab3A p25 small GTP-binding

A.Reference number: A48097; MUID:93204952; PMID:8384302

A.Accession: A48097

A.Status: preliminary; not compared with conceptual translation

A.Molecule type: nucleic acid; protein

A.Residues: 1-704 <SH>

A.Cross-references: GB:D13613; NID:9285645; PIDN:BA002780.1; PID:d1003285; PID:9285646

A.Experimental source: brain

A>Note: sequence extracted from NCBI backbone (NCBIP:127629)

C.Superfamily: protein kinase C C2 region homology
F.J396-512/Domain: protein kinase C C2 region homology <KC2A>
F.J554-669/Domain: protein kinase C C2 region homology <KC2B>

Query Match

Best Local Similarity 57.8%; Score 37; DB 2; Length 704;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DPLTKLWL 10

Db 597 DPFVKLWL 604

RESULT 77

A53714

protein kinase (EC 2.7.1.37) BL44 - human

N.Alternate names: GC kinase

C.Species: Homo sapiens (man)

C.Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Sep-1999

C.Accession: A53714

R.Katze, P.; Whalen, G.; Kehrl, J.H.

J.Biol. Chem. 269, 16802-16809, 1994

A.Title: Differential expression of a novel protein kinase in human B lymphocytes. Prefe

A.Reference number: A53714; MUID:94266900; PMID:7515885

A.Accession: A53714

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-819 <KAT>

A.Cross-references: GB:U07349; NID:9531819; PIDN:AAA20968.1; PID:9531820

C.Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo-

C.Keywords: ATP; phosphotransferase

F.I3-272/Domain: protein kinase homology <KIN>

F.I21-29/Region: protein kinase ATP-binding motif

Query Match

Best Local Similarity 57.8%; Score 37; DB 2; Length 819;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDEPLTKLWL 10

Db 626 WYEPLOKFKLL 635

RESULT 78

T37789

Scd1 protein - fission yeast (Schizosaccharomyces pombe)

C.Species: Schizosaccharomyces pombe

C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Nov-2000

C.Accession: T37789; T52490

R.Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

Submitted to the EMBL Data Library, September 1995

A.Reference number: Z21746

A.Accession: T37789

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Molecule type: DNA

A.Residues: 1-872 <OLI>

A.Cross-references: EMBL:Z99529; PIDN:CAB11037.1; GSPDB:GN00066; SPDB:SPAC16E8.09

A.Experimental source: strain 972h(-); cosmid c16E8

R.Chang, E.C.; Barr, M.; Wang, Y.; Jung, V.; Xu, H.P.; Wigler, M.H.

Cell 79, 131-141, 1994

A.Title: Cooperative interaction of S. pombe proteins required for mating and morphogene

A.Reference number: Z09915

A.Accession: T52490

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Molecule type: DNA

A.Residues: 1-872 <CHA>

A.Cross-references: EMBL:U12538; PIDN:AAA50556.2

C.Genetics: SPDB:SPAC16E8.09; scd1

A.Map position: 9/1

C.Function:

A>Description: required for normal morphology and mating

Query Match 57.8%; Score 37; DB 2; Length 872;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DPLTKLWL 10
|:|:|:|
Db 105 DPVTEIWL 112

RESULT 79

hypothetical protein DKFZp43N074.1 - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 03-Nov-2000
C:Accession: T12545
R:Mandut, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17524
A:Accession: T12545
A:Molecule type: mRNA
A:Status: preliminary
A:Residues: 1-677,678-965 <MAN>
A:Cross-references: EMBL:AL096732
A:Experimental source: adult testis; clone DKFZp43N074
A>Note: the cDNA sequence contains a -1 frameshift near codon 677
C:Genetics:
A>Note: DKFZp43N074.1
C:Superfamily: dynein heavy chain, ciliary

Query Match 57.8%; Score 37; DB 2; Length 965;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLWL 10
|:|:|:|
Db 892 YDPLPIWL 900

RESULT 80

DJBEL1
DNA-directed DNA polymerase (EC 2.7.7.7) - ictalurid herpesvirus 1 (strain auburn 1)
C:Species: ictalurid herpesvirus 1
A>Note: host ictalurid punctatus (channel catfish)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C:Accession: D36792
R:Davidson, A.J.
submitted to GenBank, January 1992
A:Description: Channel catfish virus: a new type of herpesvirus.
A:Reference number: A36804
A:Accession: D36792
A:Molecule type: DNA
A:Residues: 1-985 <DAV>
A:Cross-references: GB:M75136; NID:G331209; PIDN:AAA88160.1; PID:G331267
R:Davidson, A.J.
Virology 186, 9-14, 1992
A:Title: Channel catfish virus: a new type of herpesvirus.
A:Reference number: A39447; MUID:92087490; PMID:11727613
A:Contents: annotation
A>Note: neither amino acid nor nucleotide sequence is given
C:Genetics:
A:Gene: 57
C:Superfamily: ictalurid herpesvirus DNA-directed DNA polymerase
C:Keywords: DNA replication; nucleotidyltransferase

Query Match 57.8%; Score 37; DB 1; Length 985;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

Qy 1 WY--DPLTKLWL 10
|:|:|:|
Db 893 WVVVDPLTGIMM 904

RESULT 81
YegB protein - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 17-Mar-2003
C:Accession: B64973
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Coi

A: Rose, D.J.; Mau, B.; Siao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: B64973
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-1105 <BLAT>
A:Cross-references: GB:AE00296; GB:U00096; NID:G1788373; PIDN:AACT5128.1; PID:G1788381;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: YegB
C:Superfamily: signal transduction protein with an integral membrane domain and Pas, GGD

Query Match 57.8%; Score 37; DB 2; Length 1105;
Best Local Similarity 58.3%; Pred. No. 3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 WYDPLTKL--WL 10
|:|:|:|
Db 114 WYNPLQNLADWL 125

RESULT 82
T30291
dextranase - Streptococcus sobrinus

C:Species: Streptococcus sobrinus
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: T30291
R:Manda, S.Y.; Curtiss III, R.
J. Bacteriol. 176, 3839-3850, 1994
A:Title: Purification and characterization of Streptococcus sobrinus dextranase produced
A:Reference number: Z20810; MUID:94292401; PMID:8021165
A:Accession: T30291
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1337 <MAN>
A:Cross-references: EMBL:M06978; NID:G450640; PID:G450641; PIDN:AA21772.1

Query Match 57.8%; Score 37; DB 2; Length 1337;
Best Local Similarity 55.6%; Pred. No. 3.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WYDPLTKLW 9
|:|:|:|
Db 423 YNPTSKLW 431

RESULT 83

C75250
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000
C:Accession: C75250
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: C75250
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222 <WHI>
A:Cross-references: GB:AE002092; GB:AE000513; NID:G6460455; PIDN:AAF12174.1; PID:G646046

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2628

A:Map position: 1

C:Superfamily: Deinococcus radiodurans hypothetical protein DR2628

Query Match 57.0%; Score 36.5; DB 2; Length 222;
Best Local Similarity 72.7%; Pred. No. 68;
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 WYDPLTKLWL 10
| | | | |
DB 9 WSAPLTKLWL 19

RESULT 84

E87706

prolyl oligopeptidase family protein [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: E87706

R:Niernman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Land, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Kholmaveva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: E87706

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-723 <STO>

A:Cross-references: GB:AE005673; NID:G13425449; PIDN:AAK25649.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC3687

Query Match 57.0%; Score 36.5; DB 2; Length 723;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 YDPLTKLWL 10
| | | | |
DB 511 YDPLTKLWL 520

RESULT 85

S72842

methionine synthase meth2 - Mycobacterium leprae

N:Alternate names: B2126 Cl 157 protein

C:Species: Mycobacterium leprae

C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001

C:Accession: S72842

R:Smith, D.R.; Robinson, K.

submitted to the EMBL Data Library, November 1993

A:Description: Mycobacterium leprae cosmid B2126.

A:Reference number: S72585

A:Accession: S72842

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-867 <SMI>

A:Cross-references: EMBL:U00017; NID:G466994; PIDN:AAA17182.1; PID:G466997

C:Genetics:

A:Gene: meth2

A:Start codon: GTG

Query Match 57.0%; Score 36.5; DB 2; Length 867;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 YDPLTKLWL 10
| | | | |
DB 598 YDPLTKLWL 607

RESULT 86

E87072

hypothetical protein meth [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C:Accession: E87072

R:Coile, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho-

em, M.A.; Rutherford, K.M.

em, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: E87072

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1206 <STO>

A:Cross-references: GB:AL450380; NID:G13093228; PIDN:CAC31688.1; GSPDB:GN00147

C:Genetics:

A:Gene: meth

C:Superfamily: cobalamin-dependent methionine synthase; cobalamin-binding homology

Query Match 57.0%; Score 36.5; DB 2; Length 1206;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 YDPLTKLWL 10
| | | | |
DB 620 YDPLTKLWL 629

RESULT 87

AG1129

hypothetical protein lmo0438 [imported] - Listeria monocytogenes (strain EGD-e)

C:Species: Listeria monocytogenes

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C:Accession: AG1129

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioecker

, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fshih, H.

D.; Jones, L.M.; Karel, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Ma-

ok, C.; Schueter, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AG1129

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-205 <GLA>

A:Cross-references: GB:NC_003210; PIDN:CAC98517.1; PID:G16409815; GSPDB:GN00177

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: lmo0438

Query Match 56.2%; Score 36; DB 2; Length 205;
Best Local Similarity 44.4%; Pred. No. 76;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 9
| | | | |
DB 7 WFNGLSKMW 15

RESULT 88

I76659

pregnancy-specific glycoprotein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999

C:Accession: I76659

R:Rudert, F.; Saunders, A.M.; Thompson, J.A.; Rebstock, S.; Zimmermann, W.A.

Mamm. Genome 3, 262-273, 1992

A:Title: Characterization of murine carcinoembryonic antigen gene family members.

A:Reference number: I57007; MUID:92345715; PMID:1638085

A:Accession: I76669
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-209 <RES>
A:Cross-references: GB:M83346; NID:g200318; PIDN:AAA39917.1; PID:g200319
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA1>

Query Match 56.2%; Score 36; DB 2; Length 209;
Best Local Similarity 55.6%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
|||
Db 67 WYRGMTNLM 75

RESULT 89
T50960
related to modulation protein nobb [imported] - Neurospora crassa
N:Alternate names: protein B24P7.150
C:Species: Neurospora crassa
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, July 2000
A:Reference number: Z25286
A:Accession: T50960
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-312 <SCH>
A:Cross-references: EMBL:AL389890; GSPDB:GN00116; NCSP:B24P7.150
A:Experimental source: BAC clone B24P7; strain OR74A
C:Genetics:
A:Gene: NCSP:B24P7.150
A:Map position: 6

Query Match 56.2%; Score 36; DB 2; Length 312;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 10
|||
Db 64 WTDVLMRLM 73

RESULT 90
D64233
hypothetical protein MG302 - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C>Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 07-Dec-1999
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhmann, J.; Nguyen, D.; Uettermann, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A>Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: D64233
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-317 <TIGR>
A:Cross-references: GB:U39711; GB:I43967; NID:g1045997; PID:g1046001; TIGR:MG302
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3

Query Match 56.2%; Score 36; DB 2; Length 317;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 DPLTKLM 9

Db 11 DPLTKLM 17

RESULT 91
S59388
Probable membrane protein YLR242c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein L9672.11
C:Species: Saccharomyces cerevisiae
C>Date: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 06-Feb-1998
A:Accession: S59388
R:Johnson, D.
submitted to the EMBL Data Library, February 1995
A:Description: The sequence of S. cerevisiae cosmid 9672.
A:Reference number: S59386
A:Accession: S59388
A:Molecule type: DNA
A:Residues: 1-321 <JOH>
A:Cross-references: EMBL:U00865; NID:g662330; PID:g662341; MIPS:YLR242C
A:Experimental source: strain S288C (AB972)
C:Genetics:
A:Gene: SGD:ARY1
A:Cross-references: SGD:S0004232; MIPS:YLR242C
A:Map position: 12R
C:Keywords: transmembrane protein
F:40-56/Domain: transmembrane #status predicted <TM1>
F:218-234/Domain: transmembrane #status predicted <TM2>
F:276-292/Domain: transmembrane #status predicted <TM3>

Query Match 56.2%; Score 36; DB 2; Length 321;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 10
|||
Db 102 YDRLNRLM 110

RESULT 92
H82632
ATPase XFR1828 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: H82632
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-405 <SIM>
A:Cross-references: GB:AE004004; GB:AE003849; NID:g9106905; PIDN:AAF84634.1; GSPDB:GN001;
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvares, R.; Al
Biones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carter, H
as-Nero, E.; Docena, C.; El-Porri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Klieger, J.E.; Kuramae, E.E.; Laigri
chado, M.A.; Madeira, A.M.F.; Matukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A:Autores: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Teunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XFR1828
C:Superfamily: Neisseria meningitidis probable nucleotide-binding protein NMA1520

Query Match 56.2%; Score 36; DB 2; Length 405;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
|:|:|:|:|
Db 62 WMDRFTALM 70

RESULT 93

T47818

hypotheical protein P24G16.210 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C/Accession: T47818

R/D Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;

submitted to the Protein Sequence Database, February 2000

A/Reference number: Z24477

A/Accession: T47818

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-418 <DAN>

A/Cross-references: EMBL:AL138647

A/Experimental source: cultivar Columbia; BAC clone P24G16

C/Genetics:

A/Map position: 3

A/Note: P24G16.210

Query Match 56.2%; Score 36; DB 2; Length 418;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9
|:|:|:|:|
Db 280 YDPTNSW 287

RESULT 94

S51715

hypotheical protein - Chlamydia trachomatis (fragment)

C/Species: Chlamydia trachomatis

C/Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 11-Jan-2000

C/Accession: S51715

R/Pohlner, J.;

submitted to the EMBL Data Library, April 1994

A/Description: Sequence of the recA gene from Chlamydia trachomatis L2.

A/Reference number: S51714

A/Accession: S51715

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-419 <POH>

A/Cross-references: EMBL:Z35530; NID:G607060; PIDN:CAA83540.1; PID:G607062

C/Superfamily: Chlamydia hypotheical protein CT648

Query Match 56.2%; Score 36; DB 2; Length 419;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTK 7
|:|:|:|:|
Db 236 YDPLTK 242

RESULT 95

F71488

hypotheical protein CT648 - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C/Species: Chlamydia trachomatis

C/Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 10-Dec-1999

C/Accession: F71488

R/Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998

A/Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis

A/Reference number: A1570; MUID:9900809; PMID:9784136

A/Accession: F71488

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-424 <ARN>

A/Cross-references: GB:AE001335; GB:AE001273; NID:G3329091; PIDN:AA66825.1; PID:G332909

A/Experimental source: serotype D, strain UW-3/Cx

C/Genetics:

A/Gene: CT648

C/Superfamily: Chlamydia hypotheical protein CT648

Query Match 56.2%; Score 36; DB 2; Length 424;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTK 7
|:|:|:|:|
Db 241 YDPLTK 247

RESULT 96

A64945

Probable membrane protein b1833 - Escherichia coli (strain K-12)

C/Species: Escherichia coli

C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002

C/Accession: A64945

R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col

.A.; Rose, D.V.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A/Title: The complete genome sequence of Escherichia coli K-12.

A/Reference number: A64720; MUID:9742617; PMID:9278503

A/Accession: A64945

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-427 <BLAT>

A/Cross-references: GB:AE00277; GB:U00096; NID:G1788129; PIDN:AACT4903.1; PID:G1788137;

A/Experimental source: strain K-12, substrain MG1655

C/Superfamily: hypotheical protein H1671

C/Keywords: transmembrane protein

F/69-85/Domain: transmembrane #status predicted <TM1>

F/120-136/Domain: transmembrane #status predicted <TM2>

F/163-179/Domain: transmembrane #status predicted <TM3>

F/189-205/Domain: transmembrane #status predicted <TM4>

F/274-290/Domain: transmembrane #status predicted <TM5>

F/311-327/Domain: transmembrane #status predicted <TM6>

F/390-406/Domain: transmembrane #status predicted <TM7>

Query Match 56.2%; Score 36; DB 2; Length 427;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKML 10
|:|:|:|:|
Db 84 WGEPLHITL 93

RESULT 97

C85795

hypotheical protein Z2880 [imported] - Escherichia coli (strain O157:H7, substrain EDL93)

C/Species: Escherichia coli

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C/Accession: C85795

R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, H.

Hiller, U.; Grobeck, E.D.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A/Reference number: A85480; MUID:21074935; PMID:11206551

A/Accession: C85795

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-427 <STO>

A/Cross-references: GB:AE005174; NID:G12515883; PIDN:AA656823.1; GSPDB:GN00145; UMGF:Z288

A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:

A:Gene: Z2880
A:Superfamily: hypothetical protein H11671
Query Match 56.2%; Score 36; DB 2; Length 427;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 1 WYDPLTKLWL 10
DB 84 WGEPLHLHML 93
RESULT 98
G90946
probable membrane protein EC62543 [similarity] - Escherichia coli (strain O157:H7, subst
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
C:Accession: G90946
C:Authors: T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A59629; PMID:21156231; PMID:11258796
A:Accession: G90946
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-427 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA835966.1; PID:G13362010; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
A:Genetics:
A:Gene: EC62543
C:Superfamily: hypothetical protein H11671
Query Match 56.2%; Score 36; DB 2; Length 427;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 1 WYDPLTKLWL 10
DB 84 WGEPLHLHML 93
RESULT 99
JQ1864
hypothetical 47.0K protein - bovine adenovirus 3
C:Species: Mastadenovirus bos3 (bovine adenovirus 3)
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C:Accession: JQ1864
R:Mitral, S.K.; Prevenc, L.; Babluk, L.A.; Graham, F.L.
J. Gen. Virol. 73, 3295-3300, 1992
A:Title: Sequence analysis of bovine adenovirus type 3 early region 3 and fibre protein
A:Reference number: PQ0499; PMID:93107871; PMID:1469367
A:Accession: JQ1864
A:Molecule type: DNA
A:Residues: 1-428 <MIT>
A:Cross-references: DDBJ:D12928
A:Experimental source: strain WBR-1
A:Note: the authors described cardohydrate binding site for residue 67
Query Match 56.2%; Score 36; DB 2; Length 428;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 2 YDPLTKLWL 10
DB 66 YNPPTVLMWL 74
RESULT 100
G82847
hypothetical protein XF0106 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 14-Jul-2003

C:Accession: G82847
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; PMID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: G82847
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-460 <SIM>
A:Cross-references: GB:AE003864; GB:AE003849; NID:99104879; PIDN:AAFE2919.1; GSPDB:GN001;
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carreir, H.
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.B.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0106
C:Superfamily: alpha-L-fucosidase
Query Match 56.2%; Score 36; DB 2; Length 460;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 2 YDPLTKLWL 10
DB 180 YGPLTEWML 188

Search completed: July 12, 2004, 21:30:55
Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 21:18:31 ; Search time 11 Seconds
(without alignments)
47.337 Million cell updates/sec

Title: US-09-932-613-457
Perfect score: 64
Sequence: 1 WYDPLTKLWL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	71.9	870	1	POL_JSRV
2	43	67.2	567	1	YEDQ_SALTI
3	43	67.2	570	1	YEDQ_SALTY
4	43	67.2	888	1	POL_SMRV
5	40	62.5	584	1	IPP_HUMAN
6	40	62.5	584	1	IPP_MOUSE
7	39	60.9	176	1	KEFF_ECO57
8	39	60.9	176	1	KEFF_ECOLI
9	39	60.9	176	1	KEFF_SALTI
10	39	60.9	176	1	KEFF_SALTY
11	39	60.9	176	1	KEFF_SHIFL
12	39	60.9	177	1	KEFF_KLEAE
13	39	60.9	308	1	BEIL_SFVL
14	39	60.9	333	1	VASD_MYCSM
15	39	60.9	491	1	G6PD_RHIME
16	39	60.9	983	1	Y644_MYCLE
17	38	59.4	538	1	C1WA_HUMAN
18	38	59.4	538	1	C1WA_RAT
19	38	59.4	1195	1	METH_SYNY3
20	38	59.4	1576	1	YLK3_CABEL
21	37.5	58.6	301	1	DAPA_CORBF
22	37.5	58.6	301	1	DAPA_CORBL
23	37	57.8	316	1	YK12_CABEL
24	37	57.8	363	1	YK12_YEAST
25	37	57.8	382	1	ERK6_YEAST
26	37	57.8	384	1	YB64_SCHPO
27	37	57.8	388	1	CARA_MOUSE
28	37	57.8	681	1	RP3A_MOUSE
29	37	57.8	684	1	RP3A_RAT
30	37	57.8	694	1	RP3A_HUMAN
31	37	57.8	704	1	RP3A_BOVIN
32	37	57.8	819	1	MAK2_HUMAN
33	37	57.8	821	1	MAK2_MOUSE

34	37	57.8	872	1	SCD1_SCHPO
35	37	57.8	985	1	DPOL_HSV1
36	37	57.8	1105	1	YEGE_ECOLI
37	37	57.8	1337	1	DEXT_STROD
38	36.5	57.0	1206	1	METH_MYCLE
39	36	56.2	317	1	Y402_MYCSE
40	36	56.2	359	1	PO5L_HUMAN
41	36	56.2	359	1	PO5M_HUMAN
42	36	56.2	382	1	GAL7_TIRE
43	36	56.2	427	1	O42B_DROME
44	36	56.2	469	1	YBBS_ECOLI
45	36	56.2	503	1	AR1I_DROME
46	36	56.2	557	1	AR1I_HUMAN
47	36	56.2	620	1	KHL8_HUMAN
48	36	56.2	629	1	KHL8_MOUSE
49	36	56.2	700	1	CSLA_PEHHE
50	36	56.2	847	1	MAK5_MOUSE
51	36	56.2	850	1	DEXT_STRMU
52	36	56.2	863	1	POL_IPHA
53	36	56.2	1064	1	JMJ2_HUMAN
54	36	56.2	1276	1	PHY2_SYNY3
55	36	56.2	1337	1	JIP3_MOUSE
56	36	56.2	1369	1	MOKE_SCHPO
57	36	56.2	1115	1	VF70_MERTA
58	36	56.2	115	1	VF70_MERTA
59	35	54.7	299	1	RNHL_HUMAN
60	35	54.7	301	1	RNHL_MOUSE
61	35	54.7	306	1	PEN2_ANASP
62	35	54.7	315	1	YPOR_ACICA
63	35	54.7	329	1	V493_MYCTU
64	35	54.7	359	1	TPSB_CABEL
65	35	54.7	376	1	PYRC_THEMA
66	35	54.7	417	1	ASSY_OCEIH
67	35	54.7	424	1	ER24_SCHPO
68	35	54.7	426	1	MK08_XENLA
69	35	54.7	465	1	FTSW_MYCLE
70	35	54.7	489	1	BGAL_SULSH
71	35	54.7	489	1	BGAL_SULSH
72	35	54.7	501	1	BGAL_SULSO
73	35	54.7	501	1	BACE_HUMAN
74	35	54.7	501	1	BACE_MOUSE
75	35	54.7	501	1	BACE_RAT
76	35	54.7	524	1	Y469_MYCPN
77	35	54.7	539	1	Y469_HUMAN
78	35	54.7	564	1	YEDQ_ECO57
79	35	54.7	575	1	YEDQ_ECOLI
80	35	54.7	575	1	MIS_BOVIN
81	35	54.7	608	1	BKL3_HUMAN
82	35	54.7	752	1	CAT1_MYCPO
83	35	54.7	755	1	KHL5_HUMAN
84	35	54.7	801	1	41_XENLA
85	35	54.7	822	1	DMSA_RHOSH
86	35	54.7	843	1	EF2_BETVU
87	35	54.7	867	1	POL_BMVU
88	35	54.7	867	1	POL_SRV1
89	35	54.7	867	1	POL_SRV2
90	35	54.7	1153	1	YAK1_MOUSE
91	35	54.7	1477	1	KEIC_DROME
92	35	54.7	1941	1	UBR1_KLDTA
93	34	53.1	116	1	Y960_HARIN
94	34	53.1	161	1	SP2G_BACTK
95	34	53.1	224	1	RNH2_PYRAB
96	34	53.1	224	1	RNH2_PYRFU
97	34	53.1	227	1	PRRA_RAT
98	34	53.1	243	1	TRT1_SALTY
99	34	53.1	253	1	RNHL_ARATH
100	34	53.1	259	1	MOB2_BPT4
101	34	53.1	290	1	XTN9_ARATH
102	34	53.1	292	1	XTN9_PHRAN
103	34	53.1	309	1	SP2G_BACSU
104	34	53.1	332	1	C1WH_HUMAN
105	34	53.1	354	1	YMA3_MYCBO
106	34	53.1	365	1	GAL7_YEAST

P40995	schizosacch
P28859	italarid h
P38097	escherichia
P39653	strepococc
O49755	mycobacteri
P47544	mycoplasma
O06416	homo sapien
O09247	homo sapien
O96u11	trichoderma
O9v914	dirosophila
P76271	escherichia
O9v1k5	mus musculus
O9v981	dirosophila
O9v4x5	homo sapien
O9p299	homo sapien
P59280	mus musculus
O59288	pedobacter
O9v4k4	homo sapien
O0bpm2	mus musculus
O5v443	strepococc
P4026	hamster int
O75164	homo sapien
O55434	synechocyst
O9esm9	m c-jun-ami
O9v704	schizosacch
O58965	methanococc
O75792	homo sapien
O9cwy8	mus musculus
O8z074	anabaena sp
P07783	actinobact
O11158	mycobacteri
O20351	caenorhabdi
O9wyh0	thermotoga
O6e1e5	oceanobacil
O09195	schizosacch
O8q1b6	xenopus lae
O50186	mycobacteri
P50388	sulfolobus
P22498	sulfolobus
P56817	homo sapien
P56818	mus musculus
P56819	rattus norv
P75609	mycoplasma
O8u3p4	homo sapien
O8xb92	escherichia
P76330	escherichia
P33972	bos taurus
O08404	homo sapien
O08404	mycobacteri
O96pq4	homo sapien
P11434	xenopus lae
O57366	rhodobacter
O23755	beta vulgar
P07572	stamian maso
P04025	stamian retr
P51517	stamian retr
P52332	mus musculus
O04652	dirosophila
O60614	kluyveromyc
P44064	haemophilus
P26767	baecillus th
O9v1a9	pyrococcus
O9u036	pyrococcus
P09320	rattus norv
P22107	salmonella
O9se6	arabidopsis
B392d4	bacterioph
O81d49	arabidopsis
O41658	phaseolus a
O96t54	homo sapien
O02279	mycobacteri
P08431	saccharomyc

107	34	53.1	370	1	GALT_KLUTIA	P09580 kluyveromyc	180	33	51.6	541	1	CP67 UROFA	00061 uromyces fa
108	34	53.1	381	1	AMPC_CITRR	P05193 citrobacter	181	33	51.6	576	1	RRPO_BSPB	P09675 bacteriophi
109	34	53.1	381	1	HUPN_BRAVA	Q45247 bradyrhizob	182	33	51.6	576	1	SLRP_CAEEL	P34260 caenorhabdi
110	34	53.1	387	1	ACUC_BACSU	P39067 bacillus su	183	33	51.6	589	1	ENCL_MOUSE	Q35709 mus musculu
111	34	53.1	397	1	ASSY_Thevo	Q97a55 thermoplas	184	33	51.6	627	1	ACM2_CAEEL	Q09388 caenorhabdi
112	34	53.1	472	1	UXAC_LACIA	Q94f53 lactococcus	185	33	51.6	629	1	RA21_XENIA	Q93310 xenopus lae
113	34	53.1	518	1	BAE2_HUMAN	O9y5z0 homo sapien	186	33	51.6	631	1	RA21_HUMAN	O60216 homo sapien
114	34	53.1	518	1	YAV6_CAEEL	P34569 caenorhabdi	187	33	51.6	635	1	RA21_MOUSE	O61550 mus musculu
115	34	53.1	530	1	SYK_METUA	Q57959 methanococ	188	33	51.6	649	1	ACS2_RHIME	O92kx2 rhizobium m
116	34	53.1	533	1	SYK_METMP	O50522 methanococ	189	33	51.6	670	1	INVL_MATZE	P49175 zea mays (m
117	34	53.1	543	1	YDE3_SCHPO	Q10437 schizosacch	190	33	51.6	687	1	FBPB_ACTPL	Q44123 actinobacil
118	34	53.1	547	1	CATY_BACSU	P94377 bacillus su	191	33	51.6	696	1	Y195_SYNY3	P74101 synechocyst
119	34	53.1	549	1	YQ29_BACSU	O9ym03 bacillus an	192	33	51.6	748	1	KLH1_HUMAN	Q9t1r4 homo sapien
120	34	53.1	551	1	LIDP_ECOLI	O8xdt9 escherichia	193	33	51.6	751	1	KLH1_MOUSE	O911b4 mus musculu
121	34	53.1	551	1	LIDP_SALTI	P33231 escherichia	194	33	51.6	756	1	METE_MOUSE	O89b24 buchnera ap
122	34	53.1	551	1	LIDP_SALTI	Q822e3 salmonella	195	33	51.6	766	1	METE_PSBAB	P37703 pseudomonas
123	34	53.1	551	1	LYDP_SALTY	O82163 salmonella	196	33	51.6	825	1	TORZ_HABIN	P44798 haemophilus
124	34	53.1	551	1	SYE_ARCFU	Q23979 archaeoglob	197	33	51.6	840	1	EP2_ENTHI	Q06193 entamoeba h
125	34	53.1	570	1	SP2E_CAEEL	O10579 caenorhabdi	198	33	51.6	868	1	MCW2_YEAST	P29469 saccharomyc
126	34	53.1	579	1	YH47_CAEEL	Q09563 caenorhabdi	199	33	51.6	888	1	GLR3_RAT	P19492 rattus norv
127	34	53.1	593	1	KHL2_HUMAN	O95198 homo sapien	200	33	51.6	894	1	GLR3_HUMAN	P422c3 homo sapien
128	34	53.1	597	1	GAN_HUMAN	Q0912c0 homo sapien	201	33	51.6	916	1	SCRB_LIMPO	Q45386 limulus pol
129	34	53.1	645	1	SP5D_BACSU	Q03524 bacillus su	202	33	51.6	918	1	SCRA_LIMPO	Q25390 limulus pol
130	34	53.1	676	1	FK26_HUMAN	O9bq70 homo sapien	203	33	51.6	1015	1	CND3_HUMAN	Q2bpx3 homo sapien
131	34	53.1	786	1	DPB3_DROME	O9yhr8 drosophila	204	33	51.6	1034	1	CND3_XENIA	Q9yhb5 xenopus lae
132	34	53.1	800	1	CYRA_BACAN	P40136 bacillus an	205	33	51.6	1919	1	HAPI_RAT	P97924 rattus norv
133	34	53.1	827	1	MAKI_MOUSE	P70218 mus musculu	206	33	51.6	2241	1	TREGU_HCMVA	P16785 human cytom
134	34	53.1	833	1	MAKI_HUMAN	Q92918 homo sapien	207	33	51.6	2269	1	RRPL_SVAL	P25341 simian vtru
135	34	53.1	1049	1	CARB_SULTO	Q970u7 sulfolobus	208	33	51.6	3788	1	LYST_MOUSE	P97412 mus musculu
136	34	53.1	1051	1	CARB_SULTO	O95969 sulfolobus	209	33	51.6	3801	1	LYST_HUMAN	Q99688 homo sapien
137	34	53.1	1142	1	JAK1_HUMAN	P23458 homo sapien	210	33	51.6	6629	1	R1AB_IBVB	P7920 a replicase
138	34	53.1	1173	1	TSR1_XENIA	P34448 xenopus lae	211	33	50.8	6629	1	R1AB_IBVB	Q91qct a replicase
139	34	53.1	1271	1	BCR_HUMAN	P11274 homo sapien	212	32.5	50.8	362	1	ASD1_HUMAN	P55056 homo sapien
140	34	53.1	1612	1	RPO_ORSVS	Q84133 odontogloss	213	32.5	50.8	412	1	YG08_SCHPO	O59715 schizosacch
141	34	53.1	7124	1	R1AB_CVM2	O9y9ya m replicase	214	32.5	50.8	412	1	YG08_SYNY3	Q73001 synechocyst
142	34	53.1	7176	1	R1AB_CVMAS	P16342 m replicase	215	32	50.0	55	1	ATP8_PETMA	Q7c4a7 lampetra fl
143	34	53.1	7180	1	R1AB_CVMJH	P19751 m replicase	216	32	50.0	55	1	ATP8_PETMA	Q35537 petromyzon
144	33.5	52.3	242	1	UBIG_PASMU	O9cmi6 pasteurrella	217	32	50.0	102	1	CYAY_PASMU	P57943 pasteurrella
145	33.5	52.3	532	1	INVL_YEAST	P10594 saccharomyc	218	32	50.0	110	1	CYAY_PSRPX	O88f6 pseudomonas
146	33.5	52.3	556	1	FIBP_ADE31	P36848 human adeno	219	32	50.0	110	1	CYAY_PSRPX	O88b6 pseudomonas
147	33.5	52.3	587	1	FIBP_ADE32	O96711 human adeno	220	32	50.0	179	1	YEH6_YEAST	P39979 saccharomyc
148	33.5	52.3	2436	1	ABC2_HUMAN	O9b2c7 homo sapien	221	32	50.0	194	1	YD16_HABIN	P44159 haemophilus
149	33	51.6	168	1	PIG1_DROME	P26023 drosophila	222	32	50.0	216	1	GCH1_DEIRA	Q87y4 deiniococcus
150	33	51.6	202	1	NHAI_RHORE	P21219 rhodococcus	223	32	50.0	227	1	YG33_ARCFU	O8640 archaeglob
151	33	51.6	216	1	SPR2_IPOBA	P17716 ipomoea bat	224	32	50.0	229	1	V247_MYCPN	P75428 mycoplasma
152	33	51.6	216	1	SPR8_IPOBA	P10965 ipomoea bat	225	32	50.0	249	1	MTRD_MERTAC	O8tuo0 methanosarc
153	33	51.6	220	1	RNH2_PYRHO	O59351 pyrococcus	226	32	50.0	267	1	DWAI_SCHPO	Q10322 schizosacch
154	33	51.6	229	1	Y247_MYCGB	P47489 mycoplasma	227	32	50.0	277	1	MCRA_ECOLI	P42200 enterobacte
155	33	51.6	266	1	YDCE_ECOLI	O9av60 escherichia	228	32	50.0	294	1	TSX_ENTAE	P40786 klebsiella
156	33	51.6	292	1	XTH2_NARTH	O9av60 arabidopsis	229	32	50.0	294	1	TSX_KLEPN	P70803 arabidosp
157	33	51.6	322	1	COO3_AARTH	O4354 a hexapreny	230	32	50.0	315	1	T2AI_ANASP	Q33836 thermocoga
158	33	51.6	344	1	DCOP_DEIRA	Q97v96 deinococcus	231	32	50.0	318	1	GALT_THEMA	Q04c3 mus musculu
159	33	51.6	348	1	GAU7_ECOLI	P09148 escherichia	232	32	50.0	329	1	SPM1_MOUSE	P62225 rattus norv
160	33	51.6	357	1	LUXA_KRYAS	P18299 kryptophana	233	32	50.0	335	1	SPM1_RAT	P64266 lactobacill
161	33	51.6	376	1	MUS1_RHIME	O30569 rhizobium s	234	32	50.0	336	1	ASNA_LACDE	Q39635 corydalis s
162	33	51.6	377	1	MTB1_BRUMB	O30570 rhizobium ab	235	32	50.0	338	1	Y3BK_CORSE	P22714 salmonella
163	33	51.6	399	1	MTG1_YEAST	P33378 saccharomyc	236	32	50.0	348	1	GALT_SALTY	P22714 salmonella
164	33	51.6	403	1	SYT7_HUMAN	O43581 homo sapien	237	32	50.0	355	1	GHA2_NEUCR	O05424 neurospora
165	33	51.6	402	1	SYT7_MOUSE	Q970n7 mus musculu	238	32	50.0	360	1	DVRI_XENIA	P09534 xenopus lae
166	33	51.6	407	1	CUSB_ECOLI	O8cwa2 escherichia	239	32	50.0	372	1	LIGC_TRAVE	P20013 trameetes ve
167	33	51.6	407	1	CUSB_ECOLI	O8cwa2 escherichia	240	32	50.0	374	1	SPB8_HUMAN	Q9y5b8 homo sapien
168	33	51.6	407	1	CUSB_ECOLI	P77239 escherichia	241	32	50.0	376	1	NDK7_HUMAN	P00811 escherichia
169	33	51.6	430	1	SIIB_ECOLI	O9zhd0 salmonella	242	32	50.0	377	1	AMPC_ECOLI	P37317 bacterioph
170	33	51.6	461	1	E1IB_WHEAT	P52409 triticum ae	243	32	50.0	385	1	VINT_BSPRG	P07061 flavobacter
171	33	51.6	491	1	G6PD_BUCAL	P57405 buchnera ap	244	32	50.0	392	1	NTLC_FLASK	P07062 flavobacter
172	33	51.6	491	1	G6PD_ECOLI	P22992 escherichia	245	32	50.0	392	1	NTLC_FLASK	P07062 flavobacter
173	33	51.6	511	1	OPCG_ECOLI	O8cwa2 escherichia	246	32	50.0	395	1	NDK7_MOUSE	Q9xyl8 mus musculu
174	33	51.6	511	1	OPCG_ECOLI	O8cwa2 escherichia	247	32	50.0	395	1	NDK7_MOUSE	Q9xyl8 mus musculu
175	33	51.6	511	1	OPCG_SALTY	O8xft6 salmonella	248	32	50.0	405	1	CPXM_BACSU	Q9xyl8 mus musculu
176	33	51.6	511	1	OPCG_SHIFL	Q83t03 shigella fl	249	32	50.0	408	1	ASSY_HELMO	O8gd42 heliobacill
177	33	51.6	513	1	CORA_BACSU	P07788 bacillus su	250	32	50.0	474	1	PBBB_LACIA	O8cfc3 lactococcus
178	33	51.6	536	1	OPGD_XYLFT	Q87927 xyella fas	251	32	50.0	480	1	YBQ_YEAST	P38348 saccharomyc
179	33	51.6	537	1	OPGD_XYLFA	O9pa38 xyella fas	252	32	50.0	488	1	CBB2_YECCA	O64900 eschscholiz

ID	POL_JSRV	STANDARD	PRT	870 AA.
253	32	50.0	492	1
254	32	50.0	492	1
255	32	50.0	492	1
256	32	50.0	492	1
257	32	50.0	492	1
258	32	50.0	492	1
259	32	50.0	492	1
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263	32	50.0	492	1
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269	32	50.0	492	1
270	32	50.0	492	1
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273	32	50.0	492	1
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282	32	50.0	492	1
283	32	50.0	492	1
284	32	50.0	492	1
285	32	50.0	492	1
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288	32	50.0	492	1
289	32	50.0	492	1
290	32	50.0	492	1
291	32	50.0	492	1
292	32	50.0	492	1
293	32	50.0	492	1
294	32	50.0	492	1
295	32	50.0	492	1
296	32	50.0	492	1
297	32	50.0	492	1
298	32	50.0	492	1
299	32	50.0	492	1
300	32	50.0	492	1

ALIGNMENTS

RESULT 1

POL_JSRV STANDARD; PRT: 870 AA.

AC P31623;

DT 01-JUL-1993 (Rel. 26, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE POL polypotein (Contains: Reverse transcriptase (EC 2.7.7.49); Endonuclease).

GN Sheep pulmonary adenomatosis virus (Jaagsiekte sheep retrovirus)

OS (JSRV).

OS Viruses; Retroviral viruses; Retroviridae; Betaretrovirus.

OX NCBI_TaxId=11746;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=92333675; PubMed=1629959;

RT "Nucleotide sequence of the jaagsiekte retrovirus, an exogenous and endogenous type D and B retrovirus of sheep and goats."

RL J. Virol. 66:4930-4939(1992).

CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate

CC + [DNA] (N).

CC -1- PFM: Specific enzymatic cleavages in vivo yield mature proteins.

CC -1- MISCELLANEOUS: THIS PROTEIN IS PROBABLY EXPRESSED AS A FUSED

CC GAG-POL POLYPROTEIN BY A RIBOSOMAL FRAMESHIFTING.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC -----

CC EMBL: M80216; AAA89182.1; ALT_INIT.

CC PIR: C42740; GNMVJA.

CC HSSP: P03355; IMML.

CC InterPro: IPR001037; Integrase_C.

CC InterPro: IPR003308; Integrase_Zn.

CC InterPro: IPR002156; RNaseH.

CC InterPro: IPR001584; Rye.

CC InterPro: IPR000477; RYase.

CC Pfam: PF00552; Integrase_1.

CC Pfam: PF002022; Integrase_Zn_1.

CC Pfam: PF00075; RNaseH_1.

CC Pfam: PF00665; rve; 1.

CC Pfam: PF00078; rve; 1.

CC Transferrase; RNA-directed DNA polymerase; Hydrolyase; Nuclease;

CC Endonuclease; Polypeptide.

CC SEQUENCE 870 AA; 99312 MW; CFADEAFB879C033 CRC64;

Query Match 71.9%; Score 46; DB 1; Length 870;

Best Local Similarity 77.8%; Pred. No. 4.3;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPYTKLM 9

DB 813 WKDPITNLM 821

RESULT 2

YEDO_SALTI STANDARD; PRT: 567 AA.

AC Q825R0;

DT 28-FEB-2003 (Rel. 41, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DE Hypothetical protein yedQ.

GN YEDO OR STY2194 OR T0891.

OS Salmonella typhi.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxId=601;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CT18;

RA MEDLINE=21534947; PubMed=11677608;

RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,

RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,

RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,

RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

RA Feltham T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jasele K.,

RA Krogan A., Larsen T.S., Leather S., Moute S., O'Gaora P., Parry C.,

RA Quail M.A., Rutherford K., Simmonds W., Skelton J., Stevens K.,

RA Whitehead S., Barrrell B.G.;

RT "Complete genome sequence of a multiple drug resistant Salmonella

RT enterica serovar Typhi CT18."

RL Nature 413:848-852(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Ty2 / ATCC 700931;

RX MEDLINE=22531367; PubMed=12644504;

```
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Butland V., Kodoyianni V., Schwartz D.C., Blatner F.R.,
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and C718."
CC J. Bacteriol. 185:2330-2337(2003).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE YA1C / YFIN (E.COL1), YHCK (B.SUBTILIS)
CC FAMILY.
CC -1- SIMILARITY: Contains 1 GGDEF domain.
CC -----
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CC -----
DR EMBL; AL637272; CAD05734.1; -
DR EMBL; AE016837; AA068569.1; -
DR InterPro; IPR000160; GGDEF.
DR Pfam; PF00990; GGDEF; 1.
DR SMART; SM00267; DUF1; 1.
DR TIGRFAMs; TIGR00254; GGDEF; 1.
DR PROSITE; PS50887; GGDEF; 1.
KM Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 357 377 POTENTIAL.
FT DOMAIN 425 560 GGDEF.
SQ SEQUENCE 567 AA; 65099 MW; 9E1AE3768ADADF6D CRC64;

Query Match 67.2%; Score 43; DB 1; Length 567;
Best Local Similarity 66.7%; Pred. No. 8.8;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9
Db 396 WHDPLTKLY 404

RESULT 3
YEDQ_SALTY STANDARD; PRT; 570 AA.
AC 08ZNT5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yedQ.
GN YEDQ OR STM1987.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN NCB1
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC4142 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvoney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE YA1C / YFIN (E.COL1), YHCK (B.SUBTILIS)
CC FAMILY.
CC -1- SIMILARITY: Contains 1 GGDEF domain.
CC -----
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CC -----
DR EMBL; AE008788; ALA20897.1; -
DR StyGene; SG7272; yedQ.
DR InterPro; IPR000160; GGDEF.
DR Pfam; PF00990; GGDEF; 1.
DR SMART; SM00267; DUF1; 1.
DR TIGRFAMs; TIGR00254; GGDEF; 1.
DR PROSITE; PS50887; GGDEF; 1.
KM Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 360 380 POTENTIAL.
FT DOMAIN 428 563 GGDEF.
SQ SEQUENCE 570 AA; 65429 MW; BF8FDFCF894925 CRC64;

Query Match 67.2%; Score 43; DB 1; Length 570;
Best Local Similarity 66.7%; Pred. No. 8.9;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9
Db 399 WHDPLTKLY 407

RESULT 4
POL_SMRVH STANDARD; PRT; 888 AA.
AC P03364;
DT 21-JUN-1986 (Rel. 01, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE POL polypeptide [Contains: Reverse transcriptase (EC 2.7.7.49);
DE Endonuclease].
GN POL.
OS Squirrel monkey retrovirus (SMRV-H) (SMRV-HLB).
OC Viruses; Retroid viruses; Retroviridae; Betaretrovirus.
OX NCBI_TaxID=11856;
RN NCB1
RP SEQUENCE FROM N.A.
RC MEDLINE=89073750; PubMed=3201749;
RA Oda T., Ikeda S., Watanabe S., Hatsuoka M., Akiyama K.,
RA Mitsuoka F.;
RT "Molecular cloning, complete nucleotide sequence, and gene structure
RT of the provirus genome of a retrovirus produced in a human
RT lymphoblastoid cell line."
RL Virology 167:468-476(1988).
RN [2]
RP SEQUENCE OF 595-774 FROM N.A.
RX MEDLINE=84097535; PubMed=6197754;
RA Chiu T.-W., Callahan R., Tronick S.R., Schlom J., Aaronson S.A.;
RT "Major pol gene progenitors in the evolution of oncoviruses."
RL Science 223:364-370(1984).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA} (N).
CC -----
CC -1- PRT: Specific enzymatic cleavages in vivo yield mature proteins.
CC -----
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CC -----
DR EMBL; K01706; AAA46815.1; -
DR EMBL; M23385; AAA66453.1; ALT_INIT.
DR PIR; A05072; A05072.
DR PIR; C31827; GNLJHD.
DR HSSP; P03155; INML.
DR InterPro; IPR001037; Integrase_C.
```

DR InterPro: IPR003108; Integrase_Zn.
 DR InterPro: IPR002156; RNaseH.
 DR InterPro: IPR001584; Rve.
 DR InterPro: IPR000477; RVTse.
 DR Pfam: PF00552; Integrase; 1.
 DR Pfam: PF02022; Integrase; 1.
 DR Pfam: PF00075; rnaesh; 1.
 DR Pfam: PF00078; rvt; 1.
 DR Transferrase; RNA-directed DNA polymerase; Hydrolyase; Nuclease;
 KM Endonuclease; Polypotein.
 SQ SEQUENCE 888 AA; 99165 MW; B6B2CD09C651B98B CRC64;

Query Match
 Best Local Similarity 67.2%; Score 43; DB 1; Length 888;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
 DB 821 WRDPLTSW 829

RESULT 5
 ID IPP_HUMAN STANDARD; PRT; 584 AA.
 AC 09Y573;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Actin-binding protein IPP (MIPP protein).
 GN IPP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=99173871; PubMed=10072760;
 RA Kim I.F., Mohammedi B., Huang R.C.;
 RT "Isolation and characterization of IPP, a novel human gene encoding an
 RL Gene 228:73-83(1999).
 CC -!- FUNCTION: May play a role in organizing the actin cytoskeleton.
 CC -!- SIMILARITY: Contains 1 BTB/POZ domain.
 CC -!- SIMILARITY: Contains 6 Kelch repeats.
 CC -----
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 CC -----
 CC EMBL: AF156857; AAD39007.1; -.
 DR Genew; HGNC:6108; IPP.
 DR MIM; 147485; -.
 DR GO; GO:0015629; C:actin cytoskeleton; TAS.
 DR GO; GO:0003779; F:actin binding; TAS.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR006651; Kelch.
 DR InterPro: IPR006652; Kelch_rep.
 DR Pfam; PF00651; BTB; 1.
 DR Pfam; PF01344; Kelch; 6.
 DR PRINTS; PR00501; KELCHREPEAT.
 DR SMART; SMO0225; BTB; 1.
 DR SMART; SMO0612; Kelch; 6.
 DR PROSITE; PS50097; BTB; 1.
 KM Cytoskeleton; Actin-binding; Kelch repeat; Repeat.
 FT DOMAIN 37 104 BTB.
 FT REPEAT 289 343 KELCH 1.
 FT REPEAT 344 390 KELCH 2.

FT REPEAT 391 437 KELCH 3.
 FT REPEAT 439 485 KELCH 4.
 FT REPEAT 487 533 KELCH 5.
 FT REPEAT 535 583 KELCH 6.
 SQ SEQUENCE 584 AA; 65260 MW; C63EF25D74924AB8 CRC64;

Query Match
 Best Local Similarity 75.0%; Score 40; DB 1; Length 584;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKM 9
 DB 363 YDPVTKW 370

RESULT 6
 ID IPP_MOUSE STANDARD; PRT; 584 AA.
 AC P28575;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Actin-binding protein IPP (MIPP protein) (Murine IAP-promoted
 DE placenta-expressed protein).
 GN IPP OR MIPP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA1B/C;
 RX MEDLINE=21427516; PubMed=11536049;
 RA Vanhouten J.N., Asch H.U., Asch B.B.;
 RT "Cloning and characterization of ectopically expressed transcripts
 RT for the actin-binding protein MIPP in mouse mammary carcinomas";
 RL Oncogene 20:5366-5372(2001).
 RN [2]
 RP SEQUENCE OF 355-556 FROM N.A.
 RX MEDLINE=91305114; PubMed=1906605;
 RA Chang-Yeh A., Mold D.E., Huang R.C.C.;
 RT "Identification of a novel murine IAP-promoted placenta-expressed
 RT gene";
 RL Nucleic Acids Res. 19:3667-3672(1991).
 CC -!- FUNCTION: May play a role in organizing the actin cytoskeleton.
 CC -!- SIMILARITY: Contains 1 BTB/POZ domain.
 CC -!- SIMILARITY: Contains 6 Kelch repeats.
 CC -----
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 CC -----
 CC EMBL: AF285178; AAK00278.1; -.
 DR EMBL; X58523; CAA41413.1; -; ALT_SEQ.
 DR EMBL; X58524; CAA41414.1; -; ALT_SEQ.
 DR PIR; S16442; S16442.
 DR MGD; MGI:96581; IPP.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR006652; Kelch_rep.
 DR Pfam; PF00651; BTB; 1.
 DR Pfam; PF01344; Kelch; 6.
 DR SMART; SMO0225; BTB; 1.
 DR SMART; SMO0612; Kelch; 6.
 DR PROSITE; PS50097; BTB; 1.
 KM Cytoskeleton; Actin-binding; Kelch repeat; Repeat.
 FT DOMAIN 37 104 BTB.
 FT REPEAT 296 343 KELCH 1.
 FT REPEAT 344 390 KELCH 2.
 FT REPEAT 391 437 KELCH 3.


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CC -----
DR EMBL, D10483; BAB96514.1; -
DR EMBL, AE000115; AAC73157.1; -
DR EMBL, AE016755; AAN78552.1; -
DR PIR, P64725; P64725.
DR HSSP, P16083; 1OR2.
DR Ecogen: BG11568; keff.
DR HAMAP, MF_01414; -; 1.
DR InterPro: IPR003680; NADHdh_2.
DR Pfam: PF02525; Flavodoxin_2; 1.
DR Complete proteome.
DR CONFLICT 79 79 D -> N (IN REF. 1).
DR CONFLICT 123 123 V -> G (IN REF. 1).
SQ SEQUENCE 176 AA; 20170 MW; F641B3952F4EFC41 CRC64;

Query Match 60.9%; Score 39; DB 1; Length 176;
Best Local Similarity 58.3%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD--PLTKML 10
DB 67 WYSVPLTKML 78

RESULT 9
KEFF_SALTY STANDARD; PRT; 176 AA.
ID KEFF_SALTY
AC Q829X1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glutathione-regulated potassium-efflux system ancillary protein keff.
GN KEFF OR STY0100 OR T0088.
OS Salmomella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Churchill J., Dougan G., James K.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Comerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogan A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Lyou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- FUNCTION: Required for full activity of keff (By similarity).
CC -!- MISCELLANEOUS: It is unlikely that keff has oxidoreductase
CC activity, it has probably evolved from its function as
CC oxidoreductase to be regulator of keff.
CC -!- SIMILARITY: Belongs to the NAD(P)H dehydrogenase (quinone) family.
CC Keff subfamily.

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CC -----
DR EMBL, AL627265; CAD01241.1; -
DR EMBL, AE016834; AAC67821.1; -
DR HAMAP, MF_01414; -; 1.
DR InterPro: IPR003680; NADHdh_2.
DR Pfam: PF02525; Flavodoxin_2; 1.
DR Complete proteome.
DR CONFLICT 176 AA; 19943 MW; EC7627FB7B698027 CRC64;
SQ SEQUENCE 176 AA; 20005 MW; 9B5CF2FB7B684B55 CRC64;

Query Match 60.9%; Score 39; DB 1; Length 176;
Best Local Similarity 58.3%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD--PLTKML 10
DB 67 WYSVPLTKML 78

RESULT 10
KEFF_SALTY STANDARD; PRT; 176 AA.
ID KEFF_SALTY
AC Q829X3;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glutathione-regulated potassium-efflux system ancillary protein keff.
GN KEFF OR STY0085.
OS Salmomella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Lt2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali U., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT Lt2.";
RL Nature 413:852-856(2001).
CC -!- FUNCTION: Required for full activity of keff (By similarity).
CC -!- MISCELLANEOUS: It is unlikely that keff has oxidoreductase
CC activity, it has probably evolved from its function as
CC oxidoreductase to be regulator of keff.
CC -!- SIMILARITY: Belongs to the NAD(P)H dehydrogenase (quinone) family.
CC Keff subfamily.
CC -----
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CC -----
DR EMBL, AE008697; AAL19049.1; -
DR StGene, SG72727; keff.
DR HAMAP, MF_01414; -; 1.
DR InterPro: IPR003680; NADHdh_2.
DR Pfam: PF02525; Flavodoxin_2; 1.
DR Complete proteome.
SQ SEQUENCE 176 AA; 20005 MW; 9B5CF2FB7B684B55 CRC64;

```

Query Match 60.9%; Score 39; DB 1; Length 176;
 Best Local Similarity 58.3%; Pred. No. 13;
 Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD--PLTKLWL 10
 DB 67 WYSVPLKLKLM 78

RESULT 11

KEFP_SHIFL STANDARD; PRT; 176 AA.
 AC 0835Q4;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Glutathione-regulated potassium-efflux system ancillary protein kefp.
 GN KFP OR SF0043 OR S0045.
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 NCBI_TaxID=623;
 RX NCBI

SEQUENCE FROM N.A.
 RC STRAIN=301 / Serotype 2a;
 RX MEDLINE=22272406; PubMed=12384590;
 RA Jin Q., Yuan Z., Xu Y., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 Cheng H., Tao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 through comparison with genomes of Escherichia coli K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 [2]

SEQUENCE FROM N.A.
 RC STRAIN=2457T / ATCC 700930 / Serotype 2a;
 RX MEDLINE=22590274; PubMed=12704152;
 RA Wei U., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
 Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
 Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.D., Zhou S.,
 Schwartz D.C., Blattner F.R.;
 RT "Complete genome sequence and comparative genomics of Shigella
 flexneri serotype 2a strain 2457T.";
 RL Infect. Immun. 71:2775-2786(2003).
 CC -1- FUNCTION: Required for full activity of kefc (BY similarity).
 CC -1- MISCELLANEOUS: It is unlikely that kefp has oxidoreductase
 activity, it has probably evolved from its function as
 oxidoreductase to be regulator of kefc.
 CC -1- SIMILARITY: Belongs to the NAD(P)H dehydrogenase (quinone) family.
 CC Kefp subfamily.

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 CC -----

DR EMBL; AE015041; AAN41709.1; -;
 DR EMBL; AE016978; AAP15589.1; -;
 DR HAMAP; MF_01414; -; 1.
 DR InterPro; IPR003680; NADPH_2.
 DR Pfam; PF02525; Flavodoxin_2; 1.
 KW Complete proteome.

SEQUENCE 176 AA; 2036 MW; P84F037B2FAF66B CRC64;

Query Match 60.9%; Score 39; DB 1; Length 176;
 Best Local Similarity 58.3%; Pred. No. 13;
 Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD--PLTKLWL 10
 DB 67 WYSVPLKLKLM 78

RESULT 12

KEFP_KLEAE STANDARD; PRT; 177 AA.
 AC 09X755;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Glutathione-regulated potassium-efflux system ancillary protein kefp.
 GN KFP.
 OS Klebsiella aerogenes.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 NCBI_TaxID=28451;
 RX NCBI

SEQUENCE FROM N.A.
 RC MEDLINE=20507830; PubMed=11053405;
 RA Miller S., Ness L.S., Wood C.M., Fox B.C., Booth I.R.;
 RT "Identification of an ancillary protein, Yabp, required for activity
 of the Kefc glutathione-gated potassium efflux system in Escherichia
 coli";
 RL J. Bacteriol. 182:6536-6540(2000).
 CC -1- FUNCTION: Required for full activity of kefc (BY similarity).
 CC -1- MISCELLANEOUS: It is unlikely that kefp has oxidoreductase
 activity, it has probably evolved from its function as
 oxidoreductase to be regulator of kefc.
 CC -1- SIMILARITY: Belongs to the NAD(P)H dehydrogenase (quinone) family.
 CC Kefp subfamily.

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 CC -----
 DR EMBL; AJ242913; CAB44436.1; -;
 DR HSSP; P16083; 1QR2.
 DR HAMAP; MF_01414; -; 1.
 DR InterPro; IPR003680; NADPH_2.
 DR Pfam; PF02525; Flavodoxin_2; 1.
 KW Complete proteome.

SEQUENCE 177 AA; 20161 MW; 2D6457C4BBD7D39 CRC64;

Query Match 60.9%; Score 39; DB 1; Length 177;
 Best Local Similarity 58.3%; Pred. No. 13;
 Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD--PLTKLWL 10
 DB 67 WYSVPLKLKLM 78

RESULT 13

BE1L_SFV1 STANDARD; PRT; 308 AA.
 AC P29169;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DE BE1-1 protein.
 GN BE1-1 OR TAF.
 OS Simian foamy virus (type 1) (SFV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Spumavirinae.
 NCBI_TaxID=11964;
 RX NCBI

SEQUENCE FROM N.A.

MEDLINE=91276270; PubMed=1647358;

Kupiec J.-C., Kay A., Hayat M., Perles J., Galibert F.;

RT "Sequence analysis of the simian foamy virus type 1 genome."
RL Gene 101:185-194(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91237804; PubMed=1851862;
RA Merz A., Shaw K.E.S., Pratt-Lowe E., Barry P.A., Luciw P.A.;
RT "Identification of the simian foamy virus transcriptional
transactivator gene (taf)."
RL J. Virol. 65:2903-2909(1991).
CC -1- FUNCTION: This protein is a transcriptional transactivator.
CC -----
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CC -----
CC EMBL, X54482; -; NOT ANNOTATED_CDS.
CC -----
CC EMBL, M74039; AAA47802.1; -.
CC PIR, B39924; WMLJ51.
CC PIR, S18740; S18740.
CC InterPro: IPR004956; Foamy BEL.
CC Pfam: PF03274; Foamy BEL; 1.
CC Transcription regulation; Activator.
CC CONFLICT 89 89 D -> N (IN REF. 2).
CC CONFLICT 119 119 D -> N (IN REF. 2).
CC CONFLICT 257 257 S -> G (IN REF. 2).
CC SEQUENCE 308 AA; 35311 MW; 7E280B6EFB21D992 CRC64;
SQ
Query Match 60.9%; Score 39; DB 1; Length 308;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 2 YDPLTKLM 10
DB 155 YDPELTMV 163
RESULT 14
YASD MYCSM STANDARD; PRT; 333 AA.
AC P41602; 1-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 35.9 kDa protein in aad 3'region (ORF).
OS Mycobacterium smegmatis.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 607 / mc(2)6 / NRRL B-692;
RX MEDLINE=94254720; PubMed=7910936;
RA Citillo J.D., Weisbrod T.R., Pascoe J.L., Bloom B.R.,
RA Jacobs W.R. Jr.;
RT "Isolation and characterization of the aspartokinase and aspartate
semialdehyde dehydrogenase operon from mycobacteria";
RL Mol. Microbiol. 11:629-639(1999).
CC -----
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CC -----
CC EMBL, Z17372; CAA78987.1; -.
CC PIR, S42424; S42424.
CC Hypothetical protein.
KW

SQ SEQUENCE 333 AA; 35881 MW; C1C50D9A6DC37368 CRC64;
Query Match 60.9%; Score 39; DB 1; Length 333;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 WYDPLTKLM 9
DB 209 WGDPTALM 217
RESULT 15
G6PD RHIME STANDARD; PRT; 491 AA.
AC Q9Z352; 30-MAY-2000 (Rel. 39, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD).
GN ZWP OR R00704 OR SMC03070.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99328961; PubMed=10400573;
RA Willis L.B., Walker G.C.;
RT "A novel Sinorhizobium meliloti operon encodes an alpha-glucosidase
RT and a periplasmic-binding-protein-dependent transport system for
RT alpha-glucosides";
RL J. Bacteriol. 181:4176-4184(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Bolstad F., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godle T., Goffeau A., Kahn D., Kiss E., Lelaire V., Maury D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Rampeger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucose-
CC 1,5-lactone 6-phosphate + NADPH.
CC -1- PATHWAY: Pentose phosphate pathway; first step.
CC -1- SIMILARITY: Belongs to the glucose-6-phosphate dehydrogenase
CC family.
CC -----
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CC -----
CC EMBL, AF045609; AAD12043.1; -.
CC EMBL, AL591784; CAC45276.1; -.
CC HSSP; P11411; 1DPC;
CC InterPro: IPR001282; G6PD.
CC Pfam: PF00479; G6PD; 1.
CC Pfam: PF02781; G6PD; 1.
CC PRINTS; PR00079; G6PDHRCNASE.
CC ProDom; PD001129; G6PD; 1.
CC TIGRfams; TIGR00871; zwf; 1.
CC PROSITE; PS00069; G6P_DEHYDROGENASE; 1.
CC Oxidoreductase; NADP; Glucose metabolism; Complete proteome.
KW ACT SITE 184 184 BY SIMILARITY.
FT CONFLICT 401 401 R -> T (IN REF. 1).
FT SEQUENCE 491 AA; 55301 MW; 0D8B1AFD094E1775 CRC64;
SQ

Query Match 60.9%; Score 39; DB 1; Length 491;
 Best Local Similarity 55.6%; Pred. No. 36;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
 DB 448 WIDPILKAM 456

RESULT 16

Y644_MYCLE
 ID Y644_MYCLE STANDARD; PRT; 983 AA.
 AC O9CCM6; O32904;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 GN M0644 OR MLCB1779.46.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 NCBI_TaxId=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Duvall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 RA Holtroyd S., Hornby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L., Oliver K., Quail M.A., Rajadream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus.";
 RL Nature 409:1007-1011(2001).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the UPF0182 family.

CC -----
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 CC -----
 CC EMBL; AL583919; CAC30153.1; -
 CC EMBL; Z98271; CAB11027.1; ALT_INIT.
 CC PIR; E86989; E86989.
 CC Leptoma; M0644; -
 CC HAMAP; MF_01600; -; 1.
 CC InterPro; IPR005372; UPF0182.
 CC Pfam; PF03699; UPF0182; 1.
 CC KW Hypothetical protein; Transmembrane; Complete proteome.
 CC TRANSMEM 20 37
 CC TRANSMEM 63 85
 CC TRANSMEM 113 135
 CC TRANSMEM 169 191
 CC TRANSMEM 212 229
 CC TRANSMEM 260 277
 CC TRANSMEM 284 306
 CC TRANSMEM 983 AA; 107556 MW; BC8AA30433CA594F CRC64;
 CC SEQUENCE

Query Match 60.9%; Score 39; DB 1; Length 983;
 Best Local Similarity 55.6%; Pred. No. 73;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKML 10
 DB 666 YDPLTKVM 674

RESULT 17

ID CIVA HUMAN STANDARD; PRT; 538 AA.
 AC P57789; Q8TDK7; Q8TDK8; Q9HB59;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 GN Potassium channel subfamily K member 10 (Outward rectifying potassium
 DE channel protein TREK-2) (TREK-2 K+ channel subunit).
 GN KCNK10 OR TREK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=20435789; PubMed=10880510;
 RA Lesage F., Terrenoire C., Romey G., Lazdunski M.;
 RT "Human TREK2, a 2P domain mechano-sensitive K+ channel with multiple
 RT regulations by polyunsaturated fatty acids, lysophospholipids and Gs,
 RT G1, and Gq protein-coupled receptors.";
 RL J. Biol. Chem. 275:28398-28405(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS B AND C).
 RX MEDLINE=21896087; PubMed=11897838;
 RA Gu W., Schlichter G., Hirsch J.R., Engels H., Karschin C.,
 RA Karschin A., Destr C., Steinlein O.K., Daut J.;
 RT "Expression pattern and functional characteristics of two novel splice
 RT variants of the two-pore-domain potassium channel TREK-2.";
 RL J. Physiol. (Lond) 539:657-668(2002).

CC -1- FUNCTION. OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY
 CC ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.
 CC UNSATURATED FREE FATTY ACIDS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=A; Synonyms=TREK-2a; IsoId=P57789-1; Sequence=Displayed;
 CC Name=B; Synonyms=TREK-2b; IsoId=P57789-2; Sequence=VSP_006697;
 CC Name=C; Synonyms=TREK-2c; IsoId=P57789-3; Sequence=VSP_006698;
 CC -1- TISSUE SPECIFICITY. Abundantly expressed in pancreas and kidney
 CC and to a lower level in brain, testis, colon, and small intestine.
 CC Isoform b is strongly expressed in kidney (primarily in the
 CC proximal tubule) and pancreas, whereas isoform c is abundantly
 CC expressed in brain.
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
 CC family.
 CC -----
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 CC -----
 CC EMBL; AF279890; AAC15191.1; -
 CC EMBL; AF385399; AAL95705.1; -
 CC EMBL; AF385400; AAL95706.1; -
 CC Genew; HGNC:6273; KCNK10.
 CC MIM; 603873; -
 CC GO; GO:0005267; F:potassium channel activity; TAS.
 CC GO; GO:0006810; P:transport; TAS.
 CC InterPro; IPR003280; K+channel_2pore.
 CC InterPro; IPR001622; K+channel_pore.
 CC InterPro; IPR003976; Trek channel.
 CC PRINTS; PR01333; 2PORKCHANNEL.
 CC PRINTS; PR01499; TREKCHANNEL.
 CC Transport; Ion transport; Ionic channel; Voltage-gated channel;

KW Potassium channel; Potassium; Transmembrane; Glycoprotein;
KW Alternative splicing.
FT DOMAIN 1 71 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 72 92 POTENTIAL.
FT DOMAIN 154 180 PORE-FORMING 1 (POTENTIAL).
FT TRANSSEM 182 202 POTENTIAL.
FT DOMAIN 203 233 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 234 254 POTENTIAL.
FT DOMAIN 263 294 PORE-FORMING 2 (POTENTIAL).
FT TRANSSEM 299 319 POTENTIAL.
FT DOMAIN 320 538 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VAAPSLIC 1 12 MFFLYTDFPLSL -> MGDRTGCRSDS (in isoform B).
FT VAAPSLIC 1 12 /FTID=VSP_006697.
FT VAAPSLIC 1 12 MFFLYTDFPLSL -> MFFPIETPRKQVNDPK (in isoform C).
FT VAAPSLIC 1 12 /FTID=VSP_006698.
FT VAAPSLIC 1 12 E -> G (IN REF. 2).
FT VAAPSLIC 1 12 /FTID=VSP_006698.
FT VAAPSLIC 1 12 /FTID=VSP_006698.
SQ SEQUENCE 538 AA; 59764 MW; 8EA615B08D147FBC CRC64;
Query Match 59.4%; Score 38; DB 1; Length 538;
Best Local Similarity 50.0%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
OY 1 WYDPLTKLML 10
DB 295 WYKPLWFWMI 304
RESULT 18
C1WA_RAT STANDARD; PRT; 538 AA.
ID C1WA_RAT
AC 09JIS4;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium channel subfamily K member 10 (Outward rectifying potassium channel protein TREK-2) (TREK-2 K+ channel subunit).
GN KCNK10 OR TREK2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20298807; PubMed=10747911;
RA Bang H., Kim Y., Kim D.
RT "TREK-2, a new member of the mechanosensitive tandem-pore K+ channel family."
RT J. Biol. Chem. 275:17412-17419(2000).
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS. ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING UNSATURATED FREE FATTY ACIDS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED MAINLY IN THE CEREBELLUM, SPLEEN, AND TESTIS.
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel family.
CC -----
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CC EMBL; AF196965; AAF75132.1; -
CC InterPro; IPR003280; K+channel_2pore.

DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003976; Trek channel.
DR PRINTS; PR01333; 2PORKCHANNEL.
DR PRINTS; PR01499; TREKCHANNEL.
KW Transport; Ion transport; Ionic channel; Voltage-gated channel; Potassium channel; Potassium; Transmembrane; Glycoprotein.
FT DOMAIN 1 71 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 72 92 POTENTIAL.
FT DOMAIN 154 180 PORE-FORMING 1 (POTENTIAL).
FT TRANSSEM 182 202 POTENTIAL.
FT DOMAIN 203 233 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 234 254 POTENTIAL.
FT DOMAIN 263 294 PORE-FORMING 2 (POTENTIAL).
FT TRANSSEM 299 319 POTENTIAL.
FT DOMAIN 320 538 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 538 AA; 59880 MW; 1FF33F0AA52B9784 CRC64;
Query Match 59.4%; Score 38; DB 1; Length 538;
Best Local Similarity 50.0%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
OY 1 WYDPLTKLML 10
DB 295 WYKPLWFWMI 304
RESULT 19
METH SYN3 STANDARD; PRT; 1195 AA.
ID METH SYN3
AC 055786;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 5-methyltetrahydrofolate-homocysteine methyltransferase (EC 2.1.1.13) (Methionine synthase, vitamin-B12 dependent isozyme) (MS).
GN METH OR SLR0212.
OS Synchocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64k to 92k of the genome."
RT DNA Res. 2:153-166(1995).
RL DNA Res. 2:153-166(1995).
CC -1- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate + L-homocysteine = tetrahydrofolate + L-methionine.
CC -1- COFACTOR: Cobalamin (By similarity).
CC -1- PATHWAY: Terminal step in the de novo biosynthesis of methionine.
CC -1- SIMILARITY: Belongs to the vitamin-B12 dependent methionine synthase family.
CC -----
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CC EMBL; D64002; BAA10438.1; -
CC PIR; S76592; S76592.
DR HSP; P13009; 1BMT.
DR InterPro; IPR006158; B12-binding.
DR InterPro; IPR005759; Cofet_synth_B12.
DR InterPro; IPR000489; Dhdropt_synth.
DR InterPro; IPR004223; Met_synth_B12.
DR InterPro; IPR003726; S_methyl_trans.

```
DR Pfam; PF02310; B12-binding; 1.  
DR Pfam; PF02607; B12-binding; 2; 1.  
DR Pfam; PF02965; Met_synth_B12; 1.  
DR Pfam; PF00809; Pterin_bind; 1.  
DR Pfam; PF02574; S-methyl_trans; 1.  
KW Transferrase; Methyltransferase; Methionine biosynthesis; Vitamin B12;  
KM Cofact; Complete proteome.  
FT DOMAIN  
FT METAL  
SQ SEQUENCE 1195 AA; 132539 MW; 1D9635B1BDDB583 CRC64;  
  
Query Match  
Best Local Similarity 59.4%; Score 38; DB 1; Length 1195;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
  
Oy 2 YDPLTKL 8  
Db 611 YDPLTKL 617  
  
RESULT 20  
YLK3 CAEEL STANDARD; PRT; 1576 AA.  
AC PA195I; Q95QP7;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Putative serine/threonine-protein kinase D1044.3 in chromosome III  
GC 2.7.1.-).  
GN D1044.3.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdittida; Rhabditoidea;  
OX Rhabdittidae; Peloderae; Caenorhabditis.  
RN NCBI_TaxID=6239;  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Pauley A., Waterston R.;  
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.  
RM [2]  
RV REVISIONS, AND ALTERNATIVE SPLICING.  
RA Waterston R.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=2;  
Name=a;  
IsoId=P4195I-1; Sequence=Displayed;  
Name=b;  
IsoId=P4195I-2; Sequence=VSP_004900, VSP_004901.  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
STRONG. TO ZC64.1.  
-----  
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-----  
CC EMBL; U00065; AAK68286.1; -;  
DR EMBL; U00065; AAL27237.1; -;  
DR HSRP; Q63450; IAO6.  
DR WormPeP; D1044.3a; CE27894.  
DR WormPeP; D1044.3b; CE29743.  
DR InterPro; IPRO08938; AKM.  
DR InterPro; IPRO06149; EB_region.  
DR InterPro; IPRO00719; Prot_kinase.  
DR InterPro; IPRO08271; Ser_thr_pkin_AS.  
DR InterPro; IPRO02290; Ser_thr_pkinase.  
DR InterPro; IPRO06150; Worm_repeat_1.  
DR Pfam; PF01683; Kin; 8.  
DR Pfam; PF00063; pkinaase; 1.
```

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DR ProDom PD000001; Prot kinase; 1.  
DR SMART; SMO0220;.S.TKC;_1.  
DR SMART; SMO0289; WEI; 8.  
DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.  
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.  
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.  
KW Hydrochemical protein; Transferase; Serine/threonine-protein kinase;  
FM ATP-binding; Alternative splicing  
FT DOMAIN 431 703  
FT NP_BIND 437 445  
FT BINDING 461 461  
FT ACT_SITE 569 569  
FT VARSPDLC 1 904  
FT FT  
FT FT  
FT VARSPDIC 905 1012  
FT FT  
FT FT  
SQ SEQUENCE 1576 AA; 174677 MW; 3A1IE573EB13498 CRC64;  
  
Query Match 59.4%; Score 38; DB 1; Length 1576;  
Best Local Similarity 62.5%; Pred. No. 1.7e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0  
  
Qy 2 YDPPLTKLM 9  
Db 659 YDPLNEMW 666
```

```
RESULT 21  
DAPA_COREF STANDARD; PRT; 301 AA.  
ID DAPA_COREF Q8ROM8;  
AC 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DI 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Dihydrodipicolinate synthase [EC 4.2.1.52] (DHPS).  
GN DAPA OR CE1864.  
OS Corynebacterium efficiens.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
CC Corynebacterales; Corynebacteriaceae; Corynebacterium.  
CX NCBI_TaxId=152794;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STPAIN=YV-314 / AJ 12310 / DSM 44549 / JCM 11189;  
RA Itaya H., Kimura E., Kawahara Y., Sugimoto S.;  
RT "dapB, dapa of Corynebacterium efficiens.",  
RL Submitted (APR-2002) to the EMBL/Genbank/DDBJ databases.  
RM [2]  
RS SEQUENCE FROM N.A.  
RC STPAIN=YV-314 / AJ 12310 / DSM 44549 / JCM 11189;  
RX MEDLINE=22723752; PubMed=1840036;  
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,  
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,  
RA Gojobori T.;  
RT "Comparative complete genome sequence analysis of the amino acid  
RT replacement's responsible for the thermostability of Corynebacterium  
RT efficiens".  
RL Genome Res. 13:1572-1579(2003).  
CC -1- CATALYTIC ACTIVITY L-aspartate 4-semialdehyde + pyruvate =  
CC dihydrodipicolinate + 2 H(2)O  
CC -1- PATHWAY: Biosynthesis of diaminopimelate and lysine from aspartate  
CC semialdehyde; first step.  
CC -1- SUBUNIT: Homotrimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: Belongs to the DHDS family.
```

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB083130; BAB88823.1; -
DR EMBL: AP005220; BAC18674.1; ALT_INIT.
DR HAMAP: MF_00418; -; 1.
DR InterPro: IPR005263; DADA.
DR InterPro: IPR002220; DHDPs.
DR Pfam: PF00701; DHDPs; 1.
DR PRINTS: PR00146; DHPICNTTHASE.
DR PRODOM: PD001859; DHDPs; 1.
DR TIGRFAMs: TIGR00674; dapa; 1.
DR PROSITE: PS00665; DHDPs_1; 1.
DR PROSITE: PS00666; DHDPs_2; 1.
KW Lyase; Diaminopimelate biosynthesis; lysine biosynthesis;
KW Complete proteome.
FT ACT_SITE 173
SQ SEQUENCE 301 AA; 31450 MW; D48FC57E4F00AFA CRC64;

Query Match 58.6%; Score 37.5; DB 1; Length 301;
Best Local Similarity 53.8%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

OY 1 WY---DPLTKLWL 10
DB 193 WYSGDDPLNLVWL 205

RESULT 22
DAPA CORGL STANDARD; PRT; 301 AA.
ID DAPA CORGL
AC P19808; P40109;
DT 01-FEB-1991 (Rel. 17, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrodipicolinate synthase (EC 4.2.1.52) (DHDPs).
GN DAPA OR CGL1971.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13059 / AS019;
RX MEDLINE=91057127; PubMed=2129555;
RA Bonnasie S., Oreglia J., Sicard A.M.;
RT "Nucleotide sequence of the dapa gene from Corynebacterium
RT glutamicum."
RL Nucleic Acids Res. 18:6421-6421 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13869;
RX MEDLINE=93239702; PubMed=8478336;
RA Piabarro A., Malumbres M., Mateos L.M., Oguiza J.A., Martin J.F.;
RT "A cluster of three genes (dapa, orf2, and daps) of Brevibacterium
RT lactofermentum encodes dihydrodipicolinate synthase,
RT dihydrodipicolinate reductase, and a third polypeptide of unknown
RT function."
RL J. Bacteriol. 175:2743-2749 (1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RX "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: L-aspartate 4-semialdehyde + pyruvate =
CC dihydrodipicolinate + 2 H(2)O.
CC -1- PATHWAY: Biosynthesis of diaminopimelate and lysine from aspartate
CC semialdehyde; first step.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
```

```

CC -1- SIMILARITY: Belongs to the DHDPs family.
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CC -----
DR EMBL: X53993; CA37940.1; -
DR EMBL: Z21502; CAA79714.1; -
DR EMBL: AP005280; BAB99364.1; -
DR PIR: C40626; C40626.
DR HSSP: P05640; IDHP.
DR HAMAP: MF_00418; -; 1.
DR InterPro: IPR005263; DADA.
DR InterPro: IPR002220; DHDPs.
DR Pfam: PF00701; DHDPs; 1.
DR PRINTS: PR00146; DHPICNTTHASE.
DR PRODOM: PD001859; DHDPs; 1.
DR TIGRFAMs: TIGR00674; dapa; 1.
DR PROSITE: PS00665; DHDPs_1; 1.
DR PROSITE: PS00666; DHDPs_2; 1.
KW Lyase; Diaminopimelate biosynthesis; lysine biosynthesis;
KW Complete proteome.
FT ACT_SITE 173
FT CONFICT 266
SQ SEQUENCE 301 AA; 31261 MW; 6B803A4E82933B3 CRC64;

Query Match 58.6%; Score 37.5; DB 1; Length 301;
Best Local Similarity 53.8%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

OY 1 WY---DPLTKLWL 10
DB 193 WYSGDDPLNLVWL 205

RESULT 23
XY12 CAEEL STANDARD; PRT; 316 AA.
ID XY12 CAEEL
AC Q1123;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 35.1 kDa protein C03F11.2 in chromosome X.
GN C03F11.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RT Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: WEAK, IN THE N-TERMINUS, TO C. ELIGANS F53B1.5.
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CC -----
DR EMBL: U39744; AAK18883.1; -
DR PIR: T15395; T15395.
DR WormPep: C03F11.2; C03914.
DR InterPro: IPR001279; Blactamase-like.
DR Pfam: PF00753; lactamase_B; 1.
KW Hypothetical protein.
```

SQ SEQUENCE 316 AA; 35107 MW; 6A725FCAC21CF676 CRC64;
 Query Match 57.8%; Score 37; DB 1; Length 316;
 Best Local Similarity 66.7%; Pred. No. 50;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 WYDPLTKLM 9
 Db 301 WQTLTKLM 309
 RESULT 24
 ID MK32 YEAST STANDARD; PRT; 363 AA.
 AC P23060;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MAK32 protein.
 GN MAK32 OR YCR019W OR YCR19W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 CX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89131254; PubMed=3916862;
 RA Toh-E A., Sahaishi Y.;
 RT "The PET18 locus of *Saccharomyces cerevisiae*: a complex locus
 RT containing multiple genes."
 RL Yeast 1:159-171(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Feldmann H., Mannhaupt G., Vetter I.;
 RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Necessary for the structural stability of U-A double-
 CC stranded RNA-containing particles. Necessary for growth at 37
 CC degrees Celsius as well as for maintenance of the killer plasmid.
 CC -1- SIMILARITY: TO S.POMBE SPAC4G8.14C.
 CC -----
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 CC -----
 CC DR EMBL; X59720; CAA42310.1; -
 CC DR PIR; S19429; BVBXK2.
 CC DR Germonline; 138924; -
 CC DR SGD; S0000612; MAK32.
 CC DR GO; GO:0019048; P:virus-host interaction; IMP.
 CC FT CONFLICT 15 I -> II (IN REF. 1).
 CC FT CONFLICT 82 MISSING (IN REF. 1).
 CC SQ SEQUENCE 363 AA; 40783 MW; CFB358F8ACF5EAC6 CRC64;
 Query Match 57.8%; Score 37; DB 1; Length 363;
 Best Local Similarity 62.5%; Pred. No. 57;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 YDPLTKLM 9
 Db 325 YDPIAKTW 332
 RESULT 25
 ERG6 YEAST STANDARD; PRT; 382 AA.
 AC P25087;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-OCT-1984 (Rel. 30, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Sterol 24-C-methyltransferase (EC 2.1.1.41) (Delta(24)-sterol C-
 DE methyltransferase).
 GN ERG6 OR SED6 OR ISE1 OR LIS1 OR YML008C OR YM9571.10C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 CX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94262330; PubMed=8203167;
 RA Hardwick K.G., Pelham H.R.B.;
 RT "SED6 is identical to ERG6, and encodes a putative methyltransferase
 RT required for ergosterol synthesis."
 RL Yeast 10:265-269(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94312403; PubMed=8038180;
 RA Weljhind A.A., Beavis A.D., Trumbly R.J.;
 RT "Mutations in LIS1 (ERG6) gene confer increased sodium and lithium
 RT uptake in *Saccharomyces cerevisiae*."
 RL Biochim. Biophys. Acta 1193:107-117(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C / AB972;
 RX MEDLINE=97313268; PubMed=9169872;
 RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
 RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
 RA Jagels K., Iye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
 RA Rice P., Skelton J., Walsh S., Whitehead S., Barrall B.G.;
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome
 RT XII."
 RL Nature 387:90-93(1997).
 RN [4]
 RP SEQUENCE OF 1-257 FROM N.A.
 RX MEDLINE=91285426; PubMed=2060792;
 RA Hussain M., Lenard J.;
 RT "Characterization of PDR4, a *Saccharomyces cerevisiae* gene that
 RT confers pleiotropic drug resistance in high-copy number: identity
 RT with YAP1, encoding a transcriptional activator."
 RL Gene 101:149-152(1991).
 RN [5]
 RP ACETYLATION.
 RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
 RA Volpe T., Warner J.R., McLaughlin C.S.;
 RL Submitted (SEP-1994) to Swiss-Prot.
 CC -1- FUNCTION: Methyltransferase required for ergosterol synthesis.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 5-alpha-cholest-
 CC 8,24-dien-3-beta-ol = S-adenosyl-L-homocysteine + 24-methylene-5-
 CC alpha-cholest-8-en-3-beta-ol.
 CC -----
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 CC -----
 CC DR EMBL; X74249; CAA52308.1; -
 CC DR EMBL; 572460; AAB31378.1; -
 CC DR EMBL; 249810; CAA89944.1; -
 CC DR EMBL; X53830; CAA37826.1; -
 CC DR PIR; S42003; S42003.
 CC DR Germonline; 142538; -
 CC DR SWISS-2DPAGE; P25087; YEAST.
 CC DR SGD; S0004467; ERG6.
 CC DR GO; GO:0005811; C:lipid particle; IDA.
 CC DR InterPro; IPR001601; Methyltransferase.
 CC DR InterPro; IPR000051; SAM bind.
 CC KW Sterol biosynthesis; Transferase; Methyltransferase; Acetylation.
 CC FT INTR MET 0
 CC FT MOD RES 1 0
 CC FT CONFLICT 379 379 ACETYLATION.
 CC E -> EE (IN REF. 2).

SQ SEQUENCE 382 AA; 43299 MW; D76BA9E3D9CD71B CRC64;
 Query Match 57.8%; Score 37; DB 1; Length 382;
 Best Local Similarity 66.7%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9
 DB 285 WYDPLTKLM 293

RESULT 26
 YB64 SCHPO STANDARD; PRT; 384 AA.
 ID YB64 SCHPO
 AC 009745; 1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein C12C2.04 in chromosome II.
 GN SPC12C2.04.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OC NCBI_TaxID=4896;
 [1]
 SEQUENCE FROM N.A.
 RP STRAIN=972;
 RC MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtz S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
 RA Jones K., Jones L., Jones M., Leathers S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch B.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grymoprez B.,
 RA Welter J., Vansireels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel K., Fuchs M., Fritz C., Holzer E., Meesl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leinrich H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambolt R., Punnett B.,
 RA Goffeau A., Cadieu B., Dreano S., Gloux S., Lelaure V., Motier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -1- SIMILARITY: TO S.POMBE SPAC2E11.17.

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 CC
 CC EMBL; Z54140; CAA90817.1; -
 DR PIR; T39377; T39377.
 DR GeneDB Spombe; SPBC12C2.04; -
 KW Hypothetical protein.
 SQ SEQUENCE 384 AA; 43031 MW; 3DB5A4D615096C98 CRC64;

Query Match 57.8%; Score 37; DB 1; Length 384;
 Best Local Similarity 75.0%; Pred. No. 60;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 WYDPLTKL 8
 DB 247 WYDPLTKL 254

RESULT 27
 CARA ANASP STANDARD; PRT; 388 AA.
 ID CARA ANASP
 AC 08YX07;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-
 DE phosphate synthetase glutamine chain).
 GN CARA OR ALR1155.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OC NCBI_TaxID=103690;
 [1]
 SEQUENCE FROM N.A.
 RP MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yanada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 RT cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 CC -1- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +
 CC phosphate + L-glutamate + carbamoyl phosphate.
 CC -1- PATHWAY: Arginine biosynthesis.
 CC -1- PATHWAY: Pyrimidine biosynthesis; first step.
 CC -1- SUBUNIT: Composed of two chains; the small (or glutamine) chain
 CC promotes the hydrolysis of glutamine to ammonia, which is used by
 CC the large (or ammonia) chain to synthesize carbamoyl phosphate (by
 CC similarity).
 CC -1- SIMILARITY: Belongs to the cara family.
 CC -1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.

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 CC
 CC EMBL; AP003584; BAB73112.1; -
 DR PIR; AH1950; AH1950.
 DR HAMAP; MF_01209; -; 1.
 DR InterPro; IPR006274; CARA synth small.
 DR InterPro; IPR001317; CP synthGATase.
 DR InterPro; IPR002474; CP synthsmall.
 DR InterPro; IPR000991; GATase_1.
 DR Pfam; PF00988; CPase_sm_chain; 1.
 DR PRINTS; PR00099; CPase_1.
 DR PRINTS; PR00096; GATASE.
 DR TIGRFS; TIGR01368; CPase1small; 1.
 DR PROSITE; PS00442; GATASE_TYPE_1; 1.
 KW Arginine biosynthesis; Pyrimidine biosynthesis; ligase;
 KW Glutamine amidotransferase; Complete proteome.
 FT DOMAIN 1 192
 FT ACT SITE 193 388
 FT ACT SITE 272 272
 SQ SEQUENCE 388 AA; 42256 MW; 062A038D8F4B705E CRC64;

Query Match 57.8%; Score 37; DB 1; Length 388;
 Best Local Similarity 55.6%; Pred. No. 61;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9
Db 173 WSDPTAVW 181

RESULT 28
RP3A_MOUSE
ID RP3A_MOUSE STANDARD; PRT; 681 AA.
AC P47708;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Rabphilin-3A (Exophilin 1).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Itagaki N.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain, and Eye;
RX MEDLINE=2388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
Bosak S.A., McMan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,
Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schneringer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 1-606 FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=9512445; PubMed=7822236;
RA Inagaki N., Mizuta M., Seino S.;
RT "Cloning of a mouse Rabphilin-3A expressed in hormone-secreting
cells.";
RL J. Biochem. 116:339-342(1994).
RN [4]
RP FUNCTION: Protein transport. Probably involved with Ras-related
protein Rab-3A in synaptic vesicle traffic and/or synaptic vesicle
fusion. Could play a role in neurotransmitter release by
regulating membrane flow in the nerve terminal.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Specifically expressed in brain.
CC -1- SIMILARITY: Contains 1 FYVE-type zinc finger.
CC -1- SIMILARITY: Contains 1 Rab-binding (RabBD) domain.
CC -1- SIMILARITY: Contains 1 Rab-binding (RabBD) domain.
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or send an email to license@isb-sib.ch).

CC EMBL: BC042585; AA042585.1; -
DR EMBL: BC050883; AA050883.1; -
DR EMBL: D29965; BA06231.2; -
DR PIR: J03338; J03338.
DR HSSP: P47709; 12BD.
DR MGI: 102788; Rph3a.
DR GO: 0005515; F:protein binding; IPI.
DR InterPro: IPR000008; C2.
DR InterPro: IPR008973; C2_GALB.
DR InterPro: IPR002149; LRT.
DR InterPro: IPR003115; RPH3A_effector.
DR InterPro: IPR001565; SynaptoCagmin.
DR Pfam: PF00168; C2; 2.
DR Pfam: PF02318; RPH3A_effector; 1.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00399; STNAPTOAGMN.
DR SMART: SM00239; C2; 2.
DR PROSITE: PS00499; C2_DOMAIN_1; 2.
DR PROSITE: PS50004; C2_DOMAIN_2; 2.
DR PROSITE: PS50916; RABBD; 1.
DR PROSITE: PS50178; ZF_FYVE; 1.
KW Repeat, Synapse, Protein transport, Zinc-finger.
FT DOMAIN 40 157 RAB-BINDING.
FT ZN_FING 88 145 FYVE-TYPE.
FT DOMAIN 277 361 PRO-RICH.
FT DOMAIN 381 485 C2_DOMAIN_1.
FT DOMAIN 539 642 C2_DOMAIN_2.
SQ SEQUENCE 681 AA; 75489 MM; D09F8DD2CBB271E CRC64;

Query Match 57.8%; Score 37; DB 1; Length 681;
Best Local Similarity 75.0%; Pred. No. 1; le=02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DPLTKLML 10
Db 574 DPEVKLML 581

RESULT 29
RP3A_RAT
ID RP3A_RAT STANDARD; PRT; 684 AA.
AC P47709;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rabphilin-3A (Exophilin 1).
GN RPH3A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9503210; PubMed=7946335;
RA Li C., Takei K., Geppert M., Daniell L., Stenius K., Chapman E.R.,
Jahn R., de Camilli P., Südhof T.C.;
RT "Synaptic targeting of rabphilin-3A, a synaptic vesicle
Ca2+/phospholipid-binding protein, depends on rab3A/3C.";
RL Neuron 13:885-898(1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 44-167 IN COMPLEX WITH RAB3A.
RC TISSUE=Brain;
RX MEDLINE=99148269; PubMed=10025402;
RA Ostermeier C., Brunger A.T.;
RT "Structural basis of Rab effector specificity: crystal structure of
the small G protein Rab3A complexed with the effector domain of
rabphilin-3A.";
RL Cell 96:363-374(1999).
RN [3]
RP FUNCTION: Protein transport. Probably involved with Ras-related
protein Rab-3A in synaptic vesicle traffic and/or synaptic vesicle
fusion. Could play a role in neurotransmitter release by

regulating membrane flow in the nerve terminal.

-1- SUBUNIT: Monomer.

-1- TISSUE SPECIFICITY: Specifically expressed in brain.

-1- SIMILARITY: Contains 2 C2 domains.

-1- SIMILARITY: Contains 1 FYVE-type zinc finger.

-1- SIMILARITY: Contains 1 Rab-binding (RabBD) domain.

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CC EMBL; U12571; AAA62662.1; -

CC PIR; I58166; I58166.

CC PDB; 1ZBD; 12-APR-99.

CC PDB; 3RBB; 23-DEC-99.

CC InterPro; IPR000008; C2.

CC InterPro; IPR008973; C2_CalB.

CC InterPro; IPR002149; LRI.

CC InterPro; IPR003315; RPH3A_effector.

CC InterPro; IPR001565; Synaptotagmin.

CC InterPro; IPR00306; Znf_FYVE.

CC Pfam; PF00168; C2; 2.

CC Pfam; PF03318; RPH3A_effector; 1.

CC PRINTS; PR00360; C2DOMAIN.

CC PRINTS; PR00399; SYNAPTOTAGM.

CC SMART; SM00239; C2; 2.

CC PROSITE; PS00499; C2_DOMAIN_1; 2.

CC PROSITE; PS50004; C2_DOMAIN_2; 2.

CC PROSITE; PS50916; RABBD; 1.

CC PROSITE; PS50178; ZF_FYVE; 1.

CC Repeat; Synapse; Protein transport; Zinc-finger; 3D-structure.

CC KX DOMAIN 40 157 RAB-BINDING.

CC ZN FING 88 145 FYVE-TYPE.

CC DOMAIN 280 364 PRO-RICH.

CC DOMAIN 384 488 C2 DOMAIN 1.

CC DOMAIN 542 645 C2 DOMAIN 2.

CC HELIX 50 84

CC TURN 85 85

CC STRAND 93 93

CC TURN 103 100

CC STRAND 103 104

CC TURN 108 110

CC STRAND 112 114

CC TURN 117 119

CC STRAND 120 121

CC TURN 123 125

CC STRAND 135 137

CC STRAND 138 149

CC HELIX 150 150

CC TURN 152 155

CC HELIX 156 156

CC TURN 156 156

CC SEQUENCE 684 AA; 75832 MW; 05838BC3C7A86444 CRC64;

Query Match 57.8%; Score 37; DB 1; Length 684;

Best Local Similarity 75.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DPLTKLWL 10

DB 577 DPEVTLWL 584

RESULT 30

RP3A_HUMAN STANDARD; PRT; 694 AA.

AC Q912J0; Q96AB0; 16-OCT-2001 (Rel. 40; Created)

DT 16-OCT-2001 (Rel. 40; Last sequence update)

DT 10-OCT-2003 (Rel. 42; Last annotation update)

DE Rabphilin-3A (Exophilin 1).

GN RPH3A OR KIAA0985.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=99246063; PubMed=10231032;

RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirokawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.

RT "Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."

RT DNA Res. 6:63-70(1999).

RL [2]

RN SEQUENCE FROM N.A.

RP TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Renfold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heselt F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Falley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -1- FUNCTION: Protein transport. Probably involved with Ras-related protein Rab-3A in synaptic vesicle traffic and/or synaptic vesicle fusion. Could play a role in neurotransmitter release by regulating membrane flow in the nerve terminal (by similarity).

CC -1- SIMILARITY: Contains 2 C2 domains.

CC -1- SIMILARITY: Contains 1 FYVE-type zinc finger.

CC -1- SIMILARITY: Contains 1 Rab-binding (RabBD) domain.

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CC EMBL; AB023202; BAAT6829.1; -

CC EMBL; BC017259; AAAT7259.1; -

CC HSSP; P47709; 1ZBD.

CC InterPro; IPR000008; C2.

CC InterPro; IPR008973; C2_CalB.

CC InterPro; IPR002149; LRI.

CC InterPro; IPR003315; RPH3A_effector.

CC InterPro; IPR001565; Synaptotagmin.

CC InterPro; IPR00306; Znf_FYVE.

CC Pfam; PF00168; C2; 2.

CC Pfam; PF03318; RPH3A_effector; 1.

CC PRINTS; PR00360; C2DOMAIN.

CC PRINTS; PR00399; SYNAPTOTAGM.

CC SMART; SM00239; C2; 2.

CC PROSITE; PS00499; C2_DOMAIN_1; 2.

CC PROSITE; PS50004; C2_DOMAIN_2; 2.

CC PROSITE; PS50916; RABBD; 1.

DR PROSITE; PS50178; ZF FYVE; 1.
 KW Repeat; Synapse; Protein transport; Zinc-finger.
 FT DOMAIN 44 160 RAB-BINDING.
 FT ZN_FING 92 148 FYVE-TYPE.
 FT DOMAIN 162 375 PRO-RICH.
 FT DOMAIN 394 498 C2 DOMAIN 1.
 FT DOMAIN 552 655 C2 DOMAIN 2.
 FT CONFLICT 24 28 NDKKO -> K (IN REF. 2).
 SQ SEQUENCE 694 AA; 76872 MW; B99C43F306A04D69 CRC64;

Query Match 57.8%; Score 37; DB 1; Length 694;
 Best Local Similarity 75.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DPLTKML 10
 Db 587 DPFVKML 594

RESULT 31
 RP3A BOVIN STANDARD; PRT; 704 AA.

AC 006846;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Rabphilin-3A (Exophilin 1).
 GN RPH3A.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain;

RX MEDLINE=93204952; PubMed=8384302;
 RA Shirataki H., Kaibuchi K., Sakoda T., Kishida S., Yamaguchi T.,
 Wada K., Miyazaki M., Takai Y.,
 RT "Rabphilin-3A, a putative target protein for smg GTP-binding protein
 RT GTP-binding protein related to synaptotagmin.";
 RT Mol. Cell. Biol. 13:2061-2068(1993).
 RN [2]
 RP DOMAINS.

RX MEDLINE=94086530; PubMed=8262955;
 RA Yamaguchi T., Shirataki H., Kishida S., Miyazaki M., Nishikawa J.,
 Wada K., Numata S.-I., Kaibuchi K., Takai Y.,
 RT "Two functionally different domains of rabphilin-3A, Rab3A p25/smg
 RT p25A-binding and phospholipid- and Ca(2+)-binding domains.";
 RT J. Biol. Chem. 268:27164-27170(1993).
 CC -1- FUNCTION: Protein transport. Probably involved with Ras-related
 CC protein Rab-3A in synaptic vesicle traffic and/or synaptic
 CC vesicle fusion. Could play a role in neurotransmitter release by
 CC regulating membrane flow in the nerve terminal.
 CC -1- SUBUNIT: Monomer.
 CC -1- TISSUE SPECIFICITY: Specifically expressed in brain.
 CC -1- SIMILARITY: Contains 2 C2 domains.
 CC -1- SIMILARITY: Contains 1 FYVE-type zinc finger.
 CC -1- SIMILARITY: Contains 1 Rab-binding (RabBD) domain.

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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; D13613; BA02780.1; -;
 DR PIR; A48097; A48097.
 DR HSSP; P47709; 1ZBD.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR008973; C2_CaLB.

DR InterPro; IPR002149; LRI.
 DR InterPro; IPR00315; RPH3A effector.
 DR InterPro; IPR001565; Synaptotagmin.
 DR InterPro; IPR00206; Znf_FYVE.
 DR Pfam; PF00168; C2; 2.
 DR Pfam; PF02318; RPH3A effector; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00399; SYNAPTOTAGMIN.
 DR SMART; SM00239; C2; 2.
 DR PROSITE; PS00499; C2 DOMAIN 1; 2.
 DR PROSITE; PS00004; C2 DOMAIN 2; 2.
 DR PROSITE; PS50178; RABBD; 1.
 DR PROSITE; PS50178; ZF FYVE; 1.
 KW Repeat; Synapse; Protein transport; Zinc-finger.
 FT DOMAIN 44 161 RAB-BINDING.
 FT ZN_FING 92 149 FYVE-TYPE.
 FT FT DOMAIN 417 508 C2 DOMAIN 1.
 FT DOMAIN 577 665 C2 DOMAIN 2.
 SQ SEQUENCE 704 AA; 77977 MW; 1324D048F5F8FDD4 CRC64;

Query Match 57.8%; Score 37; DB 1; Length 704;
 Best Local Similarity 75.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DPLTKML 10
 Db 597 DPFVKML 604

RESULT 32
 MAK2 HUMAN STANDARD; PRT; 819 AA.

AC 012851;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitogen-activated protein kinase kinase kinase 2 (MEKKK 2)
 DE (MAPK/ERK kinase kinase 2) (MEK kinase kinase 2) (MEKKK 2)
 DE (germinal center kinase) (GC kinase) (Rab8 interacting protein) (B
 DE lymphocyte serine/threonine protein kinase).
 GN MAP4K2 OR RAB8IP OR GCK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.

RX MEDLINE=94266900; PubMed=7515885;
 RA Katz P., Whalen G., Kehrl J.H.,
 RT "Differential expression of a novel protein kinase in human B
 RT lymphocytes. Preferential localization in the germinal center.";
 RT J. Biol. Chem. 269:16802-16809(1994).
 RN [2]
 RP FUNCTION, AND INTERACTION WITH TRAF2 AND MAP3K1.

RX MEDLINE=2164464; PubMed=11784851;
 RA Chadee D.N., Yuasa T., Kyriakis J.M.,
 RT "Direct activation of mitogen-activated protein kinase kinase kinase
 RT MEKK1 by the Ste20p homologue GCK and the adapter protein TRAF2.";
 RT Mol. Cell. Biol. 22:737-748(2002).
 CC -1- FUNCTION: Enhances MAP3K oligomerization, which may relieve
 CC amino-terminal mediated MAP3K autoinhibition and lead to
 CC activation following autophosphorylation. May play a role in the
 CC regulation of vesicle targeting or fusion.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- COFACTOR: Magnesium.
 CC -1- SUBUNIT: Interacts with TRAF2, MAP3K1 and Rab8/Wel.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Also found as a peripheral
 CC membrane protein in the Golgi region and basolateral plasma
 CC membrane domains (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly expressed in germinal center but not
 CC mantle zone B-cells. Also expressed in lung, brain and placenta
 CC and at lower levels in other tissues examined.

```

CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -1- SIMILARITY: Contains 1 CNH domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U07349; AAA20968.1; -.
DR PIR: A53714; A53714.
DR HSSP: G63450; 1A06.
DR Genew: HGNC:6864; MAP4K2.
DR MIM: 603166; -.
DR GO: GO:0000139; C:Golgi membrane; TAS.
DR GO: GO:0005625; C:soluble fraction; TAS.
DR GO: GO:0005524; F:ATP binding; IDA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR GO: GO:0007516; P:hemocyte development; TAS.
DR GO: GO:0006955; P:immune response; TAS.
DR GO: GO:0007254; P:JNK cascade; TAS.
DR GO: GO:0006903; P:nonselective vesicle targeting; NAS.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IDA.
DR GO: GO:0006950; P:response to stress; TAS.
DR InterPro: IPR001180; Citron.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR008271; Ser Thr pkin AS.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00780; CNH; 1.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SMO0036; CNH; 1.
DR SMART: SMO0220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE NEG.
DR Transferrase: Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 15 272 PROTEIN KINASE.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 135 135 BY SIMILARITY.
SQ SEQUENCE 819 AA; 91585 MW; 4BD5102005F1653C CRC64;
Query Match 57.8%; Score 37; DB 1; Length 819;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 WYDPTKLM 10
Db 626 WYEPLOKFL 635

```

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RP LOCATION.
RC STRAIN-BALB/C;
RX MEDLINE=96209873; PubMed=8643544;
RA Ren M., Zeng J., De Lencos-Chiarandini C., Rosenfeld M., Adeenik M.,
RA Sabatini D.D.;
RT "In its active form, the GTP-binding protein rab8 interacts with a
RT stress-activated protein kinase";
RL Proc. Natl. Acad. Sci. U.S.A. 93:5151-5155(1996).
RN [2]
RP SEQUENCE OF 42-821 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nishida I., Osato N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Haegawa Y., Nogami A., Schonbach C., Gajobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenhush J.,
RA Schriml L.M., Kanapin A., Matenda H., Batatov S., Beisel K.W.,
RA Blake J.A., Brad D., Bruscia V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Guetincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kongaya A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,
RA Magdoff D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shmada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Walstedt C., Wang Y., Waranabe Y., Wells C.,
RA Wilming L.G., Wyrshaw-Boris A., Yangisawa M., Yang I., Yang L.,
RA Yuan Z., Zavoian M., Zhu Y., Zimmer A., Ziminciu P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazawa N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
CC -1- FUNCTION: Enhances MAP3K1 oligomerization, which may relieve
CC amino-terminal mediated MAP3K1 autoinhibition and lead to the
CC activation following autophosphorylation. May play a role in the
CC regulation of vesicle targeting or fusion.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- COFACTOR: Magnesium.
CC -1- SUBUNIT: Interacts with TRAF2, MAP3K1 and Rab8/Mel.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Also found as a peripheral
CC membrane protein in the Golgi region and basolateral plasma
CC membrane domains.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -1- SIMILARITY: Contains 1 CNH domain.
CC -----
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CC -----
DR EMBL: U50595; AAC52571.1; -.
DR DR HSSP: AK051036; BAC34507.1; -.
DR HSSP: G63450; 1A06.
DR MGD: MGI:1346883; Map4K2.
DR GO: GO:0005524; F:ATP binding; ISS.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; ISS.
DR GO: GO:0006903; P:nonselective vesicle targeting; IDA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; ISS.
DR GO: GO:0007243; P:protein kinase cascade; ISS.
DR InterPro: IPR001180; Citron.

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DPOL_HSV1
ID DPOL_HSV1 STANDARD; PRT: 985 AA.
AC P28859;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase (EC 2.7.7.7).
GN 57.
OS Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Ictalurid herpes-like viruses.
OX NCBI_TaxID=10401;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alburn 1;
RX MEDLINE=92087490; PubMed=1727613;
RA Davison A.J.;
RT "Channel catfish virus: a new type of herpesvirus.";
RL Virology 186:9-14(1992).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ [DNA] (N).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the DNA polymerase type-B family.
CC -----
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CC -----
DR EMBL; M75136; AA88160.1; -.
DR PIR; D36792; DUBEL1.
DR InterPro; IPR006172; DNA_pol_B.
DR InterPro; IPR006134; DNA_pol_B_dom.
DR Pfam; PF00136; DNA_pol_B_1.
DR PRINTS; PR00106; DNAPOLB.
DR SMART; SM00486; POLBc; 1.
DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
DR KMW; Transferase; DNA-directed DNA polymerase; DNA replication;
DR KMW; DNA-binding; Nuclear protein.
SQ SEQUENCE 985 AA; 113468 MW; B15C48927D73385A CRC64;

Query Match 57.8%; Score 37; DB 1; Length 985;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

Oy 1 WY--DPLTKWL 10
|: |||:|:|
Db 893 WVVVDPLTGIMW 904

RESULT 36
YEGE_ECOLI STANDARD; PRT: 1105 AA.
ID YEGE_ECOLI STANDARD; PRT: 1105 AA.
AC P38097; P76391;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yege.
GN YEGE OR B2067.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

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RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Samped G., Seki Y., Sivasubraman S., Tagami H.,
RA Takeda J., Takemoto K., Mada C., Yamamoto Y., Horuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE OF 965-1105 FROM N.A.
RX MEDLINE=85054800; PubMed=6094528;
RA Nakabeppu Y., Miyata T., Kondo H., Iwanaga S., Sekiguchi M.;
RT "Structure and expression of the alpha gene of Escherichia coli
RT involved in adaptive response to alkylating agents.";
RL J. Biol. Chem. 259:13730-13736(1984).
RN [4]
RP IDENTIFICATION.
RX MEDLINE=95075659; PubMed=7984428;
RA Borodovsky M., Rudd K.E., Koonin E.V.;
RT "Intrinsic and extrinsic approaches for detecting genes in a
RT bacterial genome.";
RL Nucleic Acids Res. 22:4756-4767(1994).
CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -1- SIMILARITY: Contains 3 PAS-associated C-terminal (PAC) domains.
CC -1- SIMILARITY: Contains 1 GDEF domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE000296; AAC75128.1; -.
DR EMBL; D90844; BAA15920.1; -.
DR EMBL; D90845; BAA15925.1; -.
DR EMBL; K02498; -. NOT_ANNOTATED_CDS.
DR PIR; B64973; B64973.
DR EcoGene; EG12396; Yege.
DR InterPro; IPR001633; EAL.
DR InterPro; IPR000160; GDEF.
DR InterPro; IPR007895; MASE1.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc_C.
DR InterPro; IPR000014; PAS_domain.
DR Pfam; PF00563; EAL; 1.
DR Pfam; PF00990; GDEF; 1.
DR Pfam; PF05231; MASE1; 1.
DR Pfam; PF00785; PAC; 3.
DR Pfam; PF00989; PAS; 2.
DR SMART; SM00267; DUF1; 1.
DR SMART; SM00052; DUF2; 1.
DR SMART; SM00086; PAC; 3.
DR SMART; SM00086; PAC; 3.
DR TIGRFAMs; TIGR00254; GDEF; 1.
DR TIGRFAMs; TIGR00229; sensory_box; 3.
DR PROSITE; PS50883; EAL; 1.
DR PROSITE; PS50887; GDEF; 1.
DR PROSITE; PS50113; PAC; 3.
DR PROSITE; PS50112; PAS; 2.
KW Hypothetical protein; Repeat; Complete proteome.
FT DOMAIN 300 370 PAS 1.
FT DOMAIN 374 426 PAC 1.

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FT DOMAIN 501 552 PAC 2-
 FT DOMAIN 553 623 PAC 2-
 FT DOMAIN 626 680 PAC 3-
 FT DOMAIN 712 845 GDEF.
 FT DOMAIN 855 1104 EAL.
 FT CONFLICT 965 966 EQ -> NS (IN REF. 3).
 SQ SEQUENCE 1105 AA; 123886 MW; 22BE64B963CE9739 CRC64;
 Query Match 57.8%; Score 37; DB 1; Length 1105;
 Best Local Similarity 58.3%; Pred. No. 1.8e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
 QY 1 WYDPLTKL--WL 10
 DB 114 WYNPLQNLADWL 125
 RESULT 37
 DEXT STRDO STANDARD; PRT; 1337 AA.
 AC P39653;
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Dextranase precursor (EC 3.2.1.11) (Alpha-1,6-glucan-6-glucanohydrolase).
 DE GN DEX.
 OS Streptococcus downei (Streptococcus sobrinus).
 OG Plasmid pYA902.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
 OX NCBI_Taxid=13117;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-36.
 RX STRAIN=6715 / UAB66;
 RA MEDLINE=94292401; PubMed=8021165;
 RA Wanda S.-Y., Curtiss R. III;
 RT "Purification and characterization of Streptococcus sobrinus dextranase produced in recombinant Escherichia coli and sequence analysis of the dextranase gene.";
 RT J. Bacteriol. 176:3839-3850(1994).
 RL CC
 CC -1- FUNCTION: MAY PLAY A ROLE IN SUCROSE-INDEPENDENT ADHERENCE TO THE PELTIC- COATED TOOTH SURFACE.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,6-alpha-D-glucosidic linkages in dextran.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (potential).
 CC -1- MISCELLANEOUS: The activity of this enzyme is optimal at pH 5.3 and at 39 degrees Celsius.
 CC -1- SIMILARITY: Belongs to family 66 of glycosyl hydrolases.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-5 is the initiator.
 CC -----
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 CC -----
 CC EMBL; M96978; AAA21772.1; -
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Hydrolyase; Glycosidase; Cell wall; Peptidoglycan-anchor; Repeat;
 KW Signal; Plasmid.
 FT SIGNAL 1 30
 FT CHAIN 31 1308 DEXTRANASE.
 FT PROPEP 1309 1337 REMOVED BY SORTAGE (POTENTIAL).
 FT SITE 1305 1309 LPXTG SORTING SIGNAL (POTENTIAL).
 FT MOD_RES 1308 1308 AMIDE-LINKED TO CELL WALL (POTENTIAL).

SQ SEQUENCE 1337 AA; 143298 MW; B494275A77A2E3D0 CRC64;
 Query Match 57.8%; Score 37; DB 1; Length 1337;
 Best Local Similarity 55.6%; Pred. No. 2.2e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WYDPLTKLW 9
 DB 423 YINPTSKLW 431
 RESULT 38
 METH MYCLE STANDARD; PRT; 1206 AA.
 AC Q49775; Q8C37; Q9S378;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13) (Methionine synthase, vitamin-B12 dependent isozyme) (MS).
 GN METH OR MLI107 OR MLCB2533.04 OR B2126_C1_157.
 OS Mycobacterium lepreae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_Taxid=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith D.R., Robison K.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Englemer K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holtroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrall B.G.;
 RA "Massive gene decay in the leprosy bacillus.";
 RT Nature 409:1007-1011(2001).
 RL CC
 CC -1- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate + L-homocysteine = tetrahydrofolate + L-methionine.
 CC -1- COFACTOR: Cobalamin (By similarity).
 CC -1- PATHWAY: Terminal step in the de novo biosynthesis of methionine.
 CC -1- SIMILARITY: Belongs to the vitamin-B12 dependent methionine synthase family.
 CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 873.
 CC -----
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 CC -----
 CC EMBL; U00017; AAA17182.1; ALT FRAM.
 DR EMBL; AL035310; CAA22918.1; ALT_INIT.
 DR EMBL; AL583921; CAC31686.1; -
 DR PIR; B87072; B87072.
 DR HSSP; P13009; 1BMT.
 DR Leproma; MLI107; -
 DR InterPro; IPR006158; B12-binding.
 DR InterPro; IPR003759; Comet synth B12.
 DR InterPro; IPR000489; Dhdropt synth.
 DR InterPro; IPR004223; Met synth B12.
 DR InterPro; IPR003726; S_methyl_Trans.
 DR Pfam; PF02310; B12-binding; 1.

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DR Pfam: PF02607; B12-binding 2; 1.
DR Pfam: PF02965; Met synt B12; 1.
DR Pfam: PF00809; Pterin_bind; 1.
DR Pfam: PF02574; S-methyl_trans; 1.
DR Transferrase; Methyltransferase; Methionine biosynthesis; Vitamin B12;
KW Cobalt; Complete proteome.
FT DOMAIN 751 830 COBALAMIN-BINDING (POTENTIAL).
FT METRL 753 753 COBALAMIN-BINDING (POTENTIAL).
SQ SEQUENCE 1206 AA; 132392 MW; 7786CE5307D7CA86 CRC64;

Query Match 57.0%; Score 36.5; DB 1; Length 1206;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 2 YDPLTKL-WL 10
DB 620 YDPLQKLMWL 629

RESULT 39
Y302_MYCGE STANDARD; PRT; 317 AA.
ID Y302_MYCGE
AC P47544;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG302.
GN MG302.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Tomb J.-F., Dougherty B.A., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RL "The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Contains 1 homeobox domain.
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CC -----
DR EMBL: U39710; AAC71524.1; -.
DR PIR: D64233; D64233.
DR TIGR: MG302; -.
DR InterPro: IPR003339; CbiQ.
DR Pfam: PF02361; CbiQ; 1.
DR Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 18 38 POTENTIAL.
FT TRANSMEM 58 78 POTENTIAL.
FT TRANSMEM 92 112 POTENTIAL.
FT TRANSMEM 130 150 POTENTIAL.
FT TRANSMEM 159 179 POTENTIAL.
FT TRANSMEM 202 222 POTENTIAL.
FT TRANSMEM 252 272 POTENTIAL.
SQ SEQUENCE 317 AA; 36667 MW; BCG9741BD5283680 CRC64;

Query Match 56.2%; Score 36; DB 1; Length 317;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 DPLTKLM 9

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DB 11 DPLTKLM 17
+
RESULT 40
ID POSL_HUMAN STANDARD; PRT; 359 AA.
AC Q06416; Q9BZV9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE POU domain, class 5, transcription factor 1-like protein 1 (Oceller
DE binding protein 3-like).
GN POU5F1P1 OR POU5FLC8 OR OTF3C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUB=Liver;
RX MEDLINE=93027160; PubMed=1408763;
RA Takeda J., Saino S., Bell G.I.;
RT "Human Oct3 gene family: cDNA sequences, alternative splicing, gene
RT organization, chromosomal location, and expression at low levels in
RT adult tissues.";
RL Nucleic Acids Res. 20:4613-4620(1992).
[2]
RP SEQUENCE FROM N.A.
RC TISSUB=Kidney;
RA van Roozendaal K.E.P., Gillis A.J.M., van Asseldonk M.,
RA Oosterhuis J.W., Looijenga L.H.J., van Zoelen B.J.J.;
RT "Identification and expression analysis of novel intron-less human
RT POU5F1/OCT3 related POU domain genes.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Belongs to the POU transcription factor family.
CC Class-5 subfamily.
CC -1- SIMILARITY: Contains 1 homeobox domain.
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CC -----
DR EMBL: Z11901; CAAT7953.1; -.
DR EMBL: AF268615; AAG53083.1; -.
DR TRANSFAC: T04471; -.
DR Genew: HGNC:9223; POU5F1P1.
DR HSSP: P20263; 10CP.
DR GO: GO:0005634; C:nucleus; TAS.
DR GO: GO:0003700; F:transcription factor activity; TAS.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
DR InterPro: IPR001356; Homebox.
DR InterPro: IPR007103; POU domain.
DR Pfam: PF00046; homeobox; 1.
DR Pfam: PF00157; pou; 1.
DR PRINTS: PR00028; POUDOMAIN.
DR ProDom: PD000010; Homeobox; 1.
DR ProDom: PD000583; POU domain; 1.
DR SMART: SM00389; HOX; 1.
DR SMART: SM00352; POU; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00035; POU_1; 1.
DR PROSITE: PS00465; POU_2; FALSE_NEG.
DR DNA-binding; Homeobox; Nuclear protein.
FT DOMAIN 138 212 POU.
FT DNA_BIND 229 288 HOMEBOX.

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FT CONFLICT 197 197 I -> M (IN REF. 2)
SQ SEQUENCE 359 AA; 38570 MW; 9FBD440CEC4DD9A CRC64;

Query Match 56.2%; Score 36; DB 1; Length 359;
Best Local Similarity 70.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 WYDPLTKLWL 10
| | | | |
Db 29 WVDPLT--WL 36

RESULT 41

POS5_HUMAN STANDARD; PRT; 359 AA.
AC Q9BZV7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE POU domain, class 5, transcription factor 1-like protein 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN NCBI_TaxID=9606;
[1]

SEQUENCE FROM N.A.

RA van Roozendaal K.E.P., Gillis A.J.M., van Asseldonk M.,
Oosterhuis J.W., Looijenga L.H.J., van Zoelen E.J.J.,
RT "Identification and expression analysis of novel intron-less human
RT POU5F1/OCT3 related POU domain genes";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Belongs to the POU transcription factor family.
CC -1- SIMILARITY: Contains 1 homeobox domain.
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DR EMBL: AF266618; AAC53085.1; -
DR HSSP: P20253; 10CP.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR000327; POU domain.
DR InterPro: IPR007103; POU_homeo.
DR Pfam: PF00046; homeobox_1.
DR Pfam: PF00157; pou_1.
DR PRINTS: PR00028; POU_DOMAIN.
DR ProDom: PD000010; Homeobox_1.
DR ProDom: PD000583; POU_domain; 1.
DR SMART: SM00389; HOX; 1.
DR SMART: SM00352; POU; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
DR PROSITE: PS00035; POU_1; 1.
DR PROSITE: PS00465; POU_2; 1.
DR DNA-binding; Homeobox; Nuclear protein.
FT DOMAIN 138 212 POU.
FT DNA BIND 229 288 HOMEBOX.
SQ SEQUENCE 359 AA; 38562 MW; C5SD9513CE3F1690 CRC64;

Query Match 56.2%; Score 36; DB 1; Length 359;
Best Local Similarity 70.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 WYDPLTKLWL 10
| | | | |
Db 29 WVDPLT--WL 36

RESULT 42

GAL7_TRIE STANDARD; PRT; 382 AA.
AC Q960U1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Galactose-1-phosphate uridylyltransferase (EC 2.7.7.12) (Gal-1-P
DE uridylyltransferase) (UDP-glucose--hexose-1-phosphate
DE uridylyltransferase).
GN GAL7.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocerales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
RN [1]

SEQUENCE FROM N.A.

RC STRAIN=QM9414 / Rut C-30;
RA Seiboth B., Hofmann G., Kubicek C.P.;
RT "Lactose metabolism and cellulase production in *Hypocrea jecorina*: the
RT gal7 (galactose-1-phosphate uridylyltransferase) gene is essential for
RT growth on galactose but not for cellulase induction";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: UDP-glucose + alpha-D-galactose 1-phosphate =
CC alpha-D-glucose 1-phosphate + UDP-galactose.
CC -1- COFACTOR: Binds 1 zinc and 1 iron ion per subunit (Potential).
CC -1- PATHWAY: Galactose metabolism; second step.
CC -1- SIMILARITY: Belongs to the galactose-1-phosphate
CC uridylyltransferase family 1.

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CC or send an email to license@isb-sib.ch).

DR EMBL: AY057108; AAL14201.1; -
DR InterPro: IPR001937; Galp_UDPtransf1.
DR InterPro: IPR005851; Galp_Utransf1.
DR InterPro: IPR005851; Galp_Utransf1.
DR InterPro: IPR005849; Galp_Utransf1.
DR Pfam: PF02744; Galp_UDP_tr_C; 1.
DR Pfam: PF01087; Galp_UDP_tr_C; 1.
DR ProDom: PD005051; Galp_UDPtransf1.
DR TIGRFAMs: TIGR00209; galT_1; 1.
DR PROSITE: PS00117; GAL_P_UDP_TRANSF_1; 1.
DR TRANSFERASE; Nucleotidyltransferase; Galactose metabolism; Zinc; Iron;
KW Metal-binding.
FT ACT SITE 198 198 NUCLEOPHILE (BY SIMILARITY).
FT METAL 55 55 ZINC (POTENTIAL).
FT METAL 196 196 ZINC (POTENTIAL).
FT METAL 214 214 IRON (POTENTIAL).
FT METAL 313 313 IRON (POTENTIAL).
FT METAL 330 330 IRON (POTENTIAL).
FT METAL 332 332 IRON (POTENTIAL).
SQ SEQUENCE 382 AA; 43780 MW; 25A08CC695C39794 CRC64;

Query Match 56.2%; Score 36; DB 1; Length 382;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLWL 10
| | | | |
Db 14 YNPLTDSWL 22

RESULT 43
O42B_DROME STANDARD; PRT; 399 AA.
ID O42B_DROME

AC 09V914; (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative odorant receptor 42b.
GN OR42B OR CG12754.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaratunga P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Burton R.C., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasler E.M.,
RA Beeson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos M., Delcher S., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hoston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jaisi M., Jaisi F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA LaSko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mestrovic G., Milshina N.V., Modarres C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sideri-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitz R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
[2]
RP REVISIONS.
RX MEDLINE=22426069; PubMed=12537572;
RA Mitra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochick S.E.,
RA Smith C.D., Tupy J.L., Whitfield J.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
CC -1- FUNCTION: Probable role in the odorant response, being an odorant
CC receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- SIMILARITY: Belongs to family Dr-or of G-protein coupled
CC receptors.
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DR EMBL: AE003785; AAF57305.2; -
DR FlyBase: FBgn003043; Or42b.
DR GO: GO:0016021; C: integral to membrane; NAS.
DR GO: GO:0004984; F: olfactory receptor activity; NAS.
DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . .; NAS.
DR GO: GO:0007608; P: olfactory coupled receptor protein signalin. . .; NAS.
DR InterPro: IPR004117; 7tm_6.
KW Pfam: PF02949; 7tm_6; 1.
KW Hypothetical protein; Transmembrane; G-protein coupled receptor;
KW Glycoprotein; Olfaction; Multigene family.
FT DOMAIN 1 45
FT TRANSMEM 46 66
FT TRANSMEM 67 83
FT TRANSMEM 84 104
FT TRANSMEM 105 140
FT TRANSMEM 141 161
FT TRANSMEM 162 178
FT TRANSMEM 179 199
FT TRANSMEM 200 268
FT TRANSMEM 269 289
FT TRANSMEM 290 292
FT TRANSMEM 293 313
FT TRANSMEM 314 356
FT TRANSMEM 357 377
FT DOMAIN 378 399
FT CAROHRD 234 234
SQ SEQUENCE 399 AA; 46074 MW; 0435B9BDEB2ED CRC64;
Query Match 56.2%; Score 36; DB 1; Length 399;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 WYDPLTKML 10
DB 176 WHDGTLLKLM 185
RESULT 44
ID YEBS_ECOLI STANDARD; PRT; 427 AA.
AC P76271; 007977; 007979;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yebs.
GN YEBS OR B183 OR Z2880 OR ECS2543.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 83334;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=9742617; PubMed=9278503;
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,

RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
 RA Mirohachi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
 RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
 RA Sivasubramanian S., Tagami H., Takeda J., Takemoto K., Wada C.,
 RA Yamamoto Y., Horikuchi T.,
 RT "A 460-kb DNA sequence of the *Escherichia coli* K-12 genome
 RT corresponding to the 4.1-50.0 min region on the linkage map.",
 RT DNA Res. 3:379-392(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=0157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Poifaj G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potomous K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.,
 RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.",
 RT Nature 409:529-533(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=0157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kihara S., Shiba T., Hattori M., Shingawa H.,
 RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*
 RT O157:H7 and genomic comparison with a laboratory strain K-12.",
 RT DNA Res. 8:11-22(2001).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- SIMILARITY: BELONGS TO THE POIA FAMILY.
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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 CC -----
 DR EMBL; AF000277; AAC74903.1; -;
 DR EMBL; D90826; BAA15641.1; -;
 DR EMBL; D90827; BAA15646.1; -;
 DR EMBL; AE005406; AAG56823.1; -;
 DR EMBL; AP002558; BAB35966.1; -;
 DR PIR; A64945; A64945.
 DR PIR; G90946; G90946.
 DR EcoGene; BG14021; yebS.
 DR InterPro; IPR005219; Cons_hypoth155.
 DR InterPro; IPR007498; PqIA.
 DR Pfam; PF04403; PqIA; 2.
 DR TIGRfam; TIGR00155; pqlA_fam; 1.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 76 96 POTENTIAL.
 FT TRANSMEM 121 141 POTENTIAL.
 FT TRANSMEM 159 179 POTENTIAL.
 FT TRANSMEM 185 205 POTENTIAL.
 FT TRANSMEM 270 290 POTENTIAL.
 FT TRANSMEM 311 331 POTENTIAL.
 FT TRANSMEM 351 371 POTENTIAL.
 FT TRANSMEM 383 403 POTENTIAL.
 SQ SEQUENCE 427 AA; 48273 MW; B506E533D86146B CRC64;

Query Match 56.2%; Score 36; DB 1; Length 427;
 Best Local Similarity 50.0%; Pred. No. 99;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 45
 AR1 MOUSE
 ID AR1 MOUSE STANDARD; PRT; 469 AA.
 AC 0921K5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Aridene-1 protein homolog (Ari-1) (ubiquitin-conjugating enzyme E2-
 DE binding protein 1) (Ubch7-binding protein) (Ubcw4-interacting protein
 DE 77) (Fragment).
 GN AR1 OR Ari OR UBCH7BP OR UBP77.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-198 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Embryo;
 RX MEDLINE=99358765; PubMed=10431818;
 RA Martinez-Noel G., Niedenthal R., Tamura T., Harbers K.;
 RT "A family of structurally related RING finger proteins interacts
 RT specifically with the ubiquitin-conjugating enzyme Ubcw4.",
 RL FEBS Lett. 454:257-261(1999).
 RN [2]
 RP SEQUENCE OF 6-469 FROM N.A.
 RX MEDLINE=20341325; PubMed=10880484;
 RA Aguilera M., Oliveros M., Martinez-Padron M., Bargas J.A., Ferrus A.;
 RT "Aridene-1: a vital Drosophila gene is required in development and
 RT defines a new conserved family of ring-finger proteins.",
 RL Genetics 155:1231-1244(2000).
 CC -1- FUNCTION: Might act as an E3 ubiquitin-protein ligase, or as part
 CC of the E3 complex, which accepts ubiquitin from specific E2
 CC ubiquitin-conjugating enzymes, such as UBE2U3/UBCw4, and then
 CC transfers it to substrates.
 CC -1- SUBUNIT: Interacts with UBE2L3.
 CC -1- SUBCELLULAR LOCATION: Mainly cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: Widely expressed.
 CC -1- SIMILARITY: Contains 2 RING-type zinc fingers.
 CC -1- SIMILARITY: Contains 1 IBR-type zinc finger.
 CC -----
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 CC -----
 DR EMBL; AF361001; AAK51471.1; -;
 DR EMBL; AJ130977; CAA10275.1; -;
 DR MGI; MGI:1344363; Arhl.
 DR GO; GO:0006511; Ubiquitin-dependent protein catabolism; IPI.
 DR InterPro; IPR002867; ZnF_C6HC.
 DR InterPro; IPR001841; ZnF_ring.
 DR Pfam; PF01485; IBR; 1.
 DR SMART; SM00647; IBR; 2.
 DR SMART; SM00184; RING; 2.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS00589; ZF_RING_2; 1.
 KW Ub1 conjugation pathway; Zinc-finger; Repeat; Coiled coil.
 FT NON_TER 1 1
 FT ZN_FING 97 146 RING-TYPE 1.
 FT ZN_FING 167 228 IBR-TYPE.
 FT ZN_FING 255 300 RING-TYPE 2.
 FT DOMAIN 344 360 COILED COIL (POTENTIAL).
 FT DOMAIN 97 165 INTERACTION WITH UBE2L3.
 FT CONFLICT 60 60 Y -> C (IN REF. 1).
 SQ SEQUENCE 469 AA; 55564 MW; 023EAD363D3C7316 CRC64;

Query Match 56.2%; Score 36; DB 1; Length 469;
 Best Local Similarity 50.0%; Pred. No. 11e+00;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

CC		ubiquitin-conjugating enzymes, such as UBE2L3/UBC9M4, and then transfer it to substrates.
CC	-1- SUBUNIT:	Interacts with UBE2L3.
CC	-1- SUBCELLULAR LOCATION:	Mainly cytoplasmic.
CC	-1- TISSUE SPECIFICITY:	Widely expressed.
CC	-1- SIMILARITY:	Contains 2 RING-type zinc fingers.
CC	-1- SIMILARITY:	Contains 1 IBR-type zinc finger.
CC		-----
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CC		-----
DR	EMBL; AJ243190;	CAB8670.1; ALT_SEQ.
DR	EMBL; AF072832;	AAD2808.1; -
DR	EMBL; BC051877;	AAS1877.1; -
DR	EMBL; AJ130976;	CAA10274.1; -
DR	EMBL; AJ008611;	CAA08817.1; -
DR	EMBL; AB014774;	BAB19786.1; -
DR	GeneID; HGNC:689;	ARRH.
DR	MTM; 605624;	-
DR	GO; GO:0000151;	Cubiquitin ligase complex; TAS.
DR	GO; GO:0019899;	F-enzyme binding; IPI.
DR	GO; GO:0019787;	P-ubiquitin-like-protein ligase activity; TAS.
DR	GO; GO:0006511;	P-ubiquitin-dependent protein catabolism; TAS.
DR	InterPro; IPRO02867;	Znf C6HC.
DR	InterPro; IPRO01841;	Znf_ring.
DR	Pfam; PF01485;	IBR; 1.
DR	SMART; SM00647;	IBR; 2.
DR	SMART; SM00184;	RING; 2.
DR	PROSITE; PS00518;	ZF_RING_1; FALSE_NEG.
DR	PROSITE; PS00589;	ZF_RING_2; 1.
KW	Ub1 conjugation pathway;	Zinc-finger. Repeat; Coiled coil.
FT	DOMAIN	10 38 ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	67 92 GLY-RICH.
FT	ZN_FING	186 235 RING-TYPE 1.
FT	ZN_FING	256 317 IBR-TYPE.
FT	ZN_FING	344 389 RING-TYPE 2.
FT	DOMAIN	433 449 COILED COIL (POTENTIAL).
FT	DOMAIN	186 254 INTERACTION WITH UBE2L3.
FT	MUTAGEN	187 188 QI-SHV: NO LOSS OF INTERACTION WITH UBE2L3.
FT	MUTAGEN	188 188 I->A: LOSS OF INTERACTION WITH UBE2L3.
FT	MUTAGEN	208 208 C->A,H: LOSS OF INTERACTION WITH UBE2L3.
FT	MUTAGEN	258 258 Y->A: NO LOSS OF INTERACTION WITH UBE2L3.
FT	CONFLICT	122 122 E->D (IN REF. 2).
FT	CONFLICT	237 237 D->N (IN REF. 3).
FT	CONFLICT	303 303 F->S (IN REF. 5).
FT	CONFLICT	309 316 ENMHDPVK->AIGMITLQ (IN REF. 5).
FT	CONFLICT	322 322 K->T (IN REF. 5).
SO	SEQUENCE	557 AA; 6418 MM; DFFEF965DADA41DC8 CRC64;
Oy	Query March	56.2%; Score 36; DB 1; Length 557;
Dz	Best Local Similarity	50.0%; Prid. No. 1,3e+02;
Dz	Matches	5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Dz	1 WYDPLTLML 10	
Dz	:	
Dz	311 WHDPVCKKWL 320	
RESULT 48		
KdLS_HUMAN	STANDARD;	PRT; 620 AA.
AC	09P2G9;	
DT	28-FEB-2003 (Rel. 41, Created)	
DT	28-FEB-2003 (Rel. 41, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	Keich-like protein 8.	

GN KHLH8 OR KIAA1378.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20181126; PubMed=10718198;
 RA Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes. XVI.
 RT The complete sequences of 150 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 7:65-73(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheeter C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Martusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Toshynski S., Carninci P., Prange C.,
 RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SIMILARITY: Contains 1 BTF/POZ domain.
 CC -1- SIMILARITY: Contains 6 Kelch repeats.
 CC -----
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 CC -----
 DR EMBL; AB037799; BAA92616.2; ALT_INIT.
 DR EMBL; BC041384; AAH41384.1; --
 DR Genew; HGNC:18644; KHLH8.
 DR InterPro; IPR000210; BTF_POZ.
 DR InterPro; IPR006651; Kelch.
 DR InterPro; IPR006652; Kelch_rep.
 DR Pfam; PF00651; BTF; 1.
 DR Pfam; PF01344; Kelch; 6.
 DR PRINTS; PR00501; KELCHREPEAT.
 DR SMART; SMO0225; BTF; 1.
 DR SMART; SMO0612; Kelch; 6.
 DR PROSITE; PSS0097; BTF; 1.
 KW Kelch repeat; Repeat.
 FT DOMAIN 67 134 BTF.
 FT REPEAT 319 366
 FT REPEAT 367 413
 FT REPEAT 415 460
 FT REPEAT 462 507
 FT REPEAT 508 554
 FT REPEAT 556 601
 FT CONFLICT 520 601
 FT SEQUENCE 620 AA; 68861 MW; 46149C52C093DD2 CRC64;
 Query Match 56.2%; Score 36; DB 1; Length 620;

Best Local Similarity 55.6%; Pred. No. 1.5e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 YDPLTKLWL 10
 Db 386 FDLPLTKWM 394
 RESULT 49
 KHLH8 MOUSE STANDARD; PRT; 629 AA.
 ID P59280;
 AC 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kelch-like protein 8.
 GN KHLH8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nishida I., Osato N., Saito R., Suzuki H., Yamakawa I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schmitt L.M., Kanapin A., Matsuda H.A., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Drigani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi S., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kologava A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelain A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Waranabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hitozane-Tsukikawa T., Komno H., Nakamura M., Sakazume N., Sato K.,
 RA Shitaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 CC -1- SIMILARITY: Contains 1 BTF/POZ domain.
 CC -1- SIMILARITY: Contains 6 Kelch repeats.
 CC -----
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 CC -----
 DR EMBL; AK049960; BAC34008.1; --
 DR MGD; MGI:2179430; Khlh8.
 DR InterPro; IPR000210; BTF_POZ.
 DR InterPro; IPR006651; Kelch.
 DR InterPro; IPR006652; Kelch_rep.
 DR Pfam; PF00651; BTF; 1.
 DR Pfam; PF01344; Kelch; 6.
 DR PRINTS; PR00501; KELCHREPEAT.

DR SMART; SMO0225; BTB; 1.
DR SMART; SMO0612; Kelch; 6.
DR PROSITE; PS50097; BTB; 1.
KW Kelch repeat; Repeat.
FT DOMAIN 76 143 BTB.
FT REPEAT 328 375 KELCH 1.
FT REPEAT 376 422 KELCH 2.
FT REPEAT 424 469 KELCH 3.
FT REPEAT 471 516 KELCH 4.
FT REPEAT 517 563 KELCH 5.
FT REPEAT 565 610 KELCH 6.
SQ SEQUENCE 629 AA; 69816 MW; 684F04801AB4934B CRC64;

Query Match 56.2%; Score 36; DB 1; Length 629;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 395 FDLTKML 403
Y 2 YDLTKML 10
D 395 FDLTKML 403

RESULT 50
CSLA PEDHE STANDARD; PRT; 700 AA.
ID _CSLA_PEDHE
AC Q59286;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Chondroitinase AC precursor (EC 4.2.2.5) (Chondroitin AC lyase)
DE Chondroitin sulfate AC lyase (Chondroitin AC eliminase).
GN CSLA OR CHNAC.
OS Pedobacter heparinum (Flavobacterium heparinum).
OC Bacteri; Bacteroidetes; Sphingobacteriales;
OC Sphingobacteriaceae; Pedobacter.
OX NCBI_Taxid=984;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13125;
RX MEDLINE=20087513; PubMed=10618199;
RA Tkalet A.L., Fluk D., Blain F., Zhang-Sun G., Laliberte M.,
RA Bennett D.C., Gu K., Zimmermann J.J.F., Su H.;
RA "Isolation and expression in Escherichia coli of csla and celb, genes
RA coding for the chondroitin sulfate-degrading enzymes chondroitinase
RA heparinum.",
RA AC and chondroitinase B, respectively, from Flavobacterium
RA heparinum.",
RA Appl. Environ. Microbiol. 66:29-35 (2000).
[2]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RP MEDLINE=99264394; PubMed=10329169;
RA Fethiere J., Eggemann B., Cygler M.;
RA "Crystal structure of chondroitin AC lyase, a representative of a
RA family of glycosaminoglycan degrading enzymes.",
RA J. Mol. Biol. 288:635-647 (1999).
[3]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RP MEDLINE=2126222; PubMed=11327856;
RA Huang W., Boju L., Tkalet A.L., Su H., Yang H.O., Gunay N.S.,
RA Linhardt R.J., Kim Y.S., Matte A., Cygler M.;
RA "Active site of chondroitin AC lyase revealed by the structure of
RA enzyme-oligosaccharide complexes and mutagenesis.",
RA Biochemistry 40:2359-2372 (2001).
CC -1- CATALYTIC ACTIVITY: Elimination degradation of polysaccharides
CC containing 1,4-beta-D-hexosaminyl and 1,3-beta-D-glucosaminyl
CC linkages to disaccharides containing 4-deoxy-beta-D-gluc-4-
CC enurosyl groups.
CC -1- COFACTOR: Binds 1 calcium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to the polysaccharide lyase family 8.
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DR EMBL; U27583; AAC8383.1; -.
DR PDB; 1CB8; 14-MAY-99.
DR PDB; 1HM2; 02-MAY-01.
DR PDB; 1HM3; 02-MAY-01.
DR PDB; 1HM4; 02-MAY-01.
DR PDB; 1HM5; 02-MAY-01.
DR InterPro; IPR008929; Chondroitin_lyas.
DR InterPro; IPR003159; Lyase_8.
DR InterPro; IPR004103; Lyase_8_C.
DR Pfam; PF02278; Lyase_8; 1.
DR Pfam; PF02884; Lyase_8_C; 1.
KW Lyase; Signal; Glycoprotein; Calcium; 3D-structure.
FT SIGNAL 1 22
FT CHAIN 23 700
FT ACT_SITE 225 225
FT ACT_SITE 234 234
FT ACT_SITE 288 288
FT METAL 405 405
FT METAL 407 407
FT METAL 416 416
FT METAL 417 417
FT CARBOHYD 328 328
FT CARBOHYD 455 455
SQ SEQUENCE 700 AA; 79693 MW; C36B608FCAFC656 CRC64;

Query Match 56.2%; Score 36; DB 1; Length 700;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 422 PTLTKW 427
Y 4 PTLTKW 9
D 422 PTLTKW 427

RESULT 51
MAKS_HUMAN STANDARD; PRT; 846 AA.
ID MAKS_HUMAN
AC Q9Y4K4; Q81YF6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitogen-activated protein kinase kinase kinase 5 (EC 2.7.1.37)
DE (MAPK/ERK kinase kinase 5) (MEK kinase kinase 5) (MEKKK 5)
DE (kinase homologous to SPK1/STR20) (KHS).
GN MAPK5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
[1]
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE
RP SPECIFICITY, AND MUTAGENESIS OF LYS-49.
RC TISSUE=T-cell;
RX MEDLINE=97190217; PubMed=9038372;
RA Tung R.M., Blenis J.;
RA "A novel human SPS1/STR20 homologue, KHS, activates jun N-terminal
RA kinase.",
RA Oncogene 14:653-659 (1997).
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strunberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diachenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [3]
 RP INTERACTION WITH CRK AND CRKL.
 RX MEDLINE=99002481; PubMed=9788432;
 RA Oenli W., Kardinal C., Ruf S., Adermann K., Groffen J., Feng G.-S.,
 RA Blenis J., Tan T.-H., Feller S.M.;
 RT "The germinal center kinase (GCK)-related protein kinases HPR1 and KHS
 RT are candidates for highly selective signal transducers of Ctk family
 RT adapter proteins.";
 RT Oncogene 17:1893-1901(1998).
 CC -1- FUNCTION: May play a role in the response to environmental stress.
 CC -1- Appears to act upstream of the c-jun N-terminal pathway.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- COFACTOR: Magnesium.
 CC -1- SUBUNIT: Interacts with both SH3 domains of the adapter proteins
 CC CRK and CRKL.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Ubiquitously expressed in all tissues
 CC examined with high levels in the ovary, testis and prostate.
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
 CC ST120 subfamily.
 CC -1- SIMILARITY: Contains 1 CNH domain.
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FT DOMAIN 512 826 CNH.
 FT MUTAGEN 49 49 K->R: LOSS OF KINASE ACTIVITY AND ABILITY
 FT CONFLICT 473 473 N->K (IN REF. 2).
 SQ SEQUENCE 846 AA; 95039 MW; B17F95196AA14E08 CRC64;
 Query Match 56.2%; Score 36; DB 1; Length 846;
 Best Local Similarity 50.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 3;
 QY 1 WYDPLTKLML 10
 DB 651 WYEPKQKFM 660
 RESULT 52
 MKS MOUSE STANDARD; PRT; 847 AA.
 ID 08BPM2; O8C3U5; O8CGF3; Q9GLW7; Q9CK73;
 AC 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mitogen-activated protein kinase kinase kinase 5 (EC 2.7.1.37)
 DE (MAPK/ERK kinase kinase 5) (MEK kinase kinase 5) (MEKKK 5).
 GN MAP4K5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=C57BL/6J; TISSUE=Fetal eye, Fetal liver, and Fetal lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochva H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Funo M., Aono H., Baldarelli R., Baren G.,
 RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee R.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Montecets P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata J., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
 RA Wyszew-Borje A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=Czech II; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner L., Shuman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helt F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant J.L., Schaeetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: May play a role in the response to environmental stress.
 CC Appears to act upstream of the c-jun N-terminal pathway (By
 similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBUNIT: Interacts with both SH3 domains of the adapter proteins
 CC CRK and CRKL (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=QBPM2-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=QBPM2-2; Sequence=VSP_050478;
 CC Note=NO experimental confirmation available;
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
 CC STE20 subfamily.
 CC -1- SIMILARITY: Contains 1 CNH domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AK019468; BAB31739.1; -
 DR EMBL: AK053775; BAC35517.1; -
 DR EMBL: AK048891; BAC39305.1; -
 DR EMBL: BC040381; AAH40381.1; ALT_INIT.
 DR EMBL: BC002309; AAH02309.1; -
 DR HSSP: P24941; 1B38.
 DR MGD: MGI:1925503; Map4k5.
 DR GO: GO:0005737; Cytoplasm; ISS.
 DR GO: GO:0005524; F-ATP binding; ISS.
 DR GO: GO:0004674; F-protein serine/threonine kinase activity; ISS.
 DR GO: GO:0006468; P-protein amino acid phosphorylation; ISS.
 DR GO: GO:0007243; P-protein kinase cascade; ISS.
 DR GO: GO:0006950; P-response to stress; ISS.
 DR InterPro: IPR001180; Citron.
 DR InterPro: IPR008271; Prot_kinase.
 DR InterPro: IPR008271; Ser_Thr_kin.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00780; CNH; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00036; CNH; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TyrKc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; FALSE NEG.
 DR ATP-binding; Transferase; Serine/threonine-protein kinase;
 KW Alternative splicing;
 KW DOMAIN
 FT NP_BIND 20 277
 FT BINDING 26 34
 FT ACT_SITE 49 49
 FT ACT_SITE 140 140
 FT DOMAIN 501 827
 FT VARSPLOC 294 312
 FT VARSPLOC 294 312
 FT CONFLICT 79 79
 FT CONFLICT 103 103
 FT CONFLICT 118 118
 FT CONFLICT 441 441
 FT CONFLICT 727 727
 FT SEQUENCE 847 AA; 95044 MW; 3770E9FC6ECPA3 CRC64;

Query Match 56.2%; Score 36; DB 1; Length 847;
 Best local similarity 50.0%; Pred. No. 2e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 WYDPLTKLML 10
 DB 652 WYEPWQKFMFL 661
 RESULT 53
 DEXT_STRMU STANDARD; PRT; 850 AA.
 AC Q54443;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dextranase precursor (EC 3.2.1.11) (Alpha-1,6-glucan-6-
 GN glucanohydrolase).
 OS DEXA OR SMU.2042.
 OC Streptococcus mutans.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1309;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ingbritt;
 RX MEDLINE=96245544; PubMed=8657012;
 RA Igasaki T., Yamamoto A., Goto N.;
 RT "Sequence analysis of the Streptococcus mutans Ingbritt dexa gene
 RT encoding extracellular dextranase.";
 RL Microbiol. Immunol. 39:853-860(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ingbritt;
 RX MEDLINE=96081507; PubMed=8535521;
 RA Colby S.M., Whiting G.C., Tao L., Russell R.R.B.;
 RT "Insertional inactivation of the Streptococcus mutans dexa
 RT (dextranase) gene results in altered adherence and dextran
 RT catabolism.";
 RL Microbiology 141:2929-2936(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UA159 / ATCC 700610 / Serotype C;
 RX MEDLINE=22295063; PubMed=12397186;
 RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
 RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
 RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
 RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
 RT pathogen.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
 CC -1- FUNCTION: MAY PLAY A ROLE IN SUCROSE-INDEPENDENT ADHERENCE TO THE
 CC PELICLE-COATED TOOTH SURFACE.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,6-alpha-D-glucosidic
 CC linkages in dextran.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (potential).
 CC -1- SIMILARITY: Belongs to family 66 of glycosyl hydrolases.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D49430; BAA08409.1; -
 DR EMBL: AE015026; AAN59642.1; -
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR TIGRFAMs: TIGR01167; LPXtg_anchor; 1.

DR PROSITE: PS50847; GRAM_POS ANCHORING; 1.
 KW Hydrolase; Glycosidase; Cell wall; Peptidoglycan-anchor; Signal;
 KW Complete proteome.
 FT SIGNAL 1 ? 814 DEXTRANSASE.
 FT CHAIN 815 850 REMOVED BY SORTASE (POTENTIAL).
 FT SITE 811 815 LPTXG SORTING SIGNAL (POTENTIAL).
 FT MOD_RES 814 814 AMIDE-LINKED TO CELL WALL (POTENTIAL).
 FT CONFLICT 16 16 A -> N (IN REF. 1 AND 2).
 FT CONFLICT 22 22 T -> A (IN REF. 1 AND 2).
 FT CONFLICT 39 39 V -> A (IN REF. 1 AND 2).
 FT CONFLICT 56 56 G -> E (IN REF. 1 AND 2).
 FT CONFLICT 67 67 S -> P (IN REF. 1 AND 2).
 FT CONFLICT 141 141 A -> V (IN REF. 1 AND 2).
 FT CONFLICT 376 376 N -> T (IN REF. 1 AND 2).
 FT CONFLICT 504 504 V -> I (IN REF. 1 AND 2).
 FT CONFLICT 704 704 A -> T (IN REF. 1 AND 2).
 FT CONFLICT 707 707 I -> V (IN REF. 1 AND 2).
 FT CONFLICT 776 778 VDE -> BDG (IN REF. 1 AND 2).
 FT CONFLICT 783 783 I -> L (IN REF. 1 AND 2).
 FT CONFLICT 849 849 K -> N (IN REF. 1 AND 2).
 SQ SEQUENCE 850 AA; 94482 MW; FCF3E7DF7B4EA178 CRC64;
 Query Match 56.2%; Score 36; DB 1; Length 850;
 Best Local Similarity 55.6%; Pred. No. 2e+02; Mismatches 1; Indels 0; Gaps 0;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 OY 1 WYDPLTKLM 9
 DB 354 YYNPLSKSM 362
 RESULT 54
 ID POL_IPHA STANDARD; PRT; 863 AA.
 AC P04026;
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative POL polypeptide [contains: Endonuclease; Reverse
 DE transcripase (EC 2.7.7.49)].
 GN POL.
 OS Hamster; Retroviral a-particle (IAP-H18).
 OC Viruses; Retroviral viruses; Retroviridae; Intracisternal A-particles.
 OC NCBI_TaxID=11752;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85264989; PubMed=2991563;
 RA Ono M., Toh H., Miyata T., Awaya T.;
 RT "Nucleotide sequence of the Syrian hamster intracisternal A-particle
 RT gene: close evolutionary relationship of type A particle gene to
 RT types B and D oncovirus genes.";
 RL J. Virol. 55:387-394(1985).
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + [DNM] (N).
 CC -1- MISCELLANEOUS: READTHROUGH OF THREE TERMINATORS MAY OCCUR: TAA
 CC BETWEEN CODONS ATT FOR 660-ILE AND AAA FOR 661-LYS, TAG BETWEEN
 CC CODONS TCC FOR 832-SER AND TAT FOR 833-TYR, AND TAG BETWEEN CODONS
 CC CCC FOR 859-PRO AND ATT FOR 860-ILE.
 DR PIR: A03964; GNMVH.
 DR HSSP: P03355; IMML.
 DR InterPro: IPR001037; Integrase_C.
 DR InterPro: IPR003308; Integrase_Zn.
 DR InterPro: IPR002156; RNaseH.
 DR InterPro: IPR001584; Rve.
 DR InterPro: IPR000477; RYase.
 DR Pfam: PF00552; Integrase_1.
 DR Pfam: PF00022; Integrase_Zn_1.
 DR Pfam: PF00075; RNaseH_1.
 DR Pfam: PF00665; rve; 1.
 DR Pfam: PF00078; rvc; 1.
 KW Transferrase; RNA-directed DNA polymerase; Hydrolase; Nuclease;
 KW Endonuclease; Polypeptide.

SQ SEQUENCE 863 AA; 97036 MW; 704AE7FC6B1D86 CRC64;
 Query Match 56.2%; Score 36; DB 1; Length 863;
 Best Local Similarity 56.7%; Pred. No. 2e+02; Mismatches 3; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 WYDPLTKLM 9
 DB 764 WKDVLTDLM 772
 RESULT 55
 ID JMJ2 HUMAN STANDARD; PRT; 1064 AA.
 AC O75164;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Jmonji domain containing protein 2.
 GN JMD2 OR KIAA0677.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98403880; PubMed=9734811;
 RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
 RA Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:169-176(1998).
 [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Umed T.B., Toshimiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heltan E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SIMILARITY: Contains 1 JMD2 domain.
 CC -1- SIMILARITY: Contains 2 Tudor domains.
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 CC EMBL: AB014577; BAA31652.1;
 DR EMBL: BC002558; AA02558.1;
 DR Genew; HGNC:22978; JMD2.

```
DR InterPro: IPR003347; TF_JmjC.
DR InterPro: IPR003349; TF_JmjN.
DR InterPro: IPR002999; Tudor.
DR InterPro: IPR001965; Zn_PHD.
DR Pfam: PF02373; JmjC; 1.
DR SMART: SM002375; JmjC; 1.
DR SMART: SM00558; JmjC; 1.
DR SMART: SM00545; JmjN; 1.
DR SMART: SM00249; PHD; 2.
DR SMART: SM00333; Tudor; 2.
DR PROSITE: PS03034; Tudor; FALSE_NEG.
DR Repeat.
FT DOMAIN 13 60 JmjN.
FT DOMAIN 142 308 JmjC.
FT DOMAIN 897 954 Tudor 1.
FT DOMAIN 955 1011 Tudor 2.
SQ SEQUENCE 1064 AA; 120719 MW; 54A1BC0E579C78A CRC64;

Query Match 56.2%; Score 36; DB 1; Length 1064;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 1 WYDPLTKLW 9
Db 636 WAKPLSQLW 644

RESULT 56
PHY2_SVNY3 STANDARD; PRT; 1276 AA.
AC 055434;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phytochrome-like protein cpn2 (Bacteriophytochrome cpn2).
GN CPH2 OR SL0821.
OS Synchocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hikosawa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136 (1996).
RN [3]
RP CHROMOPHORE 1 BINDING, AND MUTAGENESIS OF CYS-129 AND HIS-130.
RX MEDLINE=20435261; PubMed=10978170;
RA Park C.-M., Kim J.-I., Yang S.-S., Kang J.-G., Kang J.-H., Shim J.-Y.,
RA Chung Y.-H., Park Y.-M., Song P.-S.;
RT "A second photochromic bacteriophytochrome from Synchocystis sp. PCC
RT 6803: spectral analysis and down-regulation by light.";
RL Biochemistry 39:10840-10847 (2000).
RN [4]
RP IDENTIFICATION OF TWO BILIN LYASE DOMAINS.
RX MEDLINE=20519044; PubMed=11063585;
RA Wu S.-H., Lagarias J.C.;
RT "Defining the bilin lyase domain: lessons from the extended
RT Phytochrome superfamily.";
RL Biochemistry 39:13487-13495 (2000).
CC -1- FUNCTION: PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE
CC REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE R FORM THAT ABSORBS
CC MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE FR FORM THAT
CC ABSORBS MAXIMALLY IN THE FAR-RED REGION.
CC -1- DOMAIN: Both bilin lyase domains bind with the bilin tetrapyrrole
CC chromophore precursor. The domain 1 shows red, far-red light
CC photoconvertibility. The domain 2 is photochemically inactive.
CC -1- SIMILARITY: Belongs to the phytochrome family.
CC -1- SIMILARITY: Contains 1 EAL domain.
CC -1- SIMILARITY: Contains 2 GGDEF domains.
CC -----
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CC -----
DR EMBL: D64003; BA10536.1; --
DR PIR: S75801; S75801.
DR InterPro: IPR001633; EAL.
DR InterPro: IPR003018; GAF.
DR InterPro: IPR00160; GGDEF.
DR InterPro: IPR01294; Phytochrome.
DR Pfam: PF00563; EAL; 1.
DR Pfam: PF01580; GAF; 3.
DR Pfam: PF00990; GGDEF; 2.
DR PRINTS: PR01033; PHYTOCHROME.
DR SMART: SM00267; DUF1; 2.
DR SMART: SM00052; DUF2; 1.
DR SMART: SM00065; GAF; 3.
DR TIGRFAMs: TIGR00254; GGDEF; 2.
DR PROSITE: PS50883; EAL; 1.
DR PROSITE: PS50887; GGDEF; 2.
DR PROSITE: PS00245; PHYTOCHROME_1; FALSE_NEG.
DR PROSITE: PS50046; PHYTOCHROME_2; 2.
KW Photoreceptor; Phytochrome; Chromophore; Repeat; Complete proteome.
FT DOMAIN 1 197
FT DOMAIN 461 598
FT DOMAIN 607 861
FT DOMAIN 939 1075
FT DOMAIN 1130 1266
FT BINDING 129 129
FT BINDING 1022 1022
FT BINDING 129 129
FT MUTAGEN 130 130
FT MUTAGEN 130 130
SQ SEQUENCE 1276 AA; 144686 MW; 318CF3A73962D99E CRC64;
Query Match 56.2%; Score 36; DB 1; Length 1276;
Best Local Similarity 63.6%; Pred. No. 3e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

Cy 2 YDPLTKL-WL 10
Db 433 YDPLTKLPNWL 443

RESULT 57
UTP3_MOUSE STANDARD; PRT; 1337 AA.
AC Q9ESN9; Q9ESK7; Q9EC08; Q9ESN7; Q9ESN8; Q9ESF0; Q9ULH2; Q9ULH3;
AC Q9R0U7;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
```

10-OCT-2003 (Rel. 42, Last annotation update)
 DE C-Jun-amino-terminal kinase interacting protein 3 (JNK-interacting
 DE protein 3) (JIP-3) (JNK MAP kinase scaffold protein 3) (Mitogen-
 DE activated protein kinase 8-interacting protein 3) (JNK/SAPK-associated
 DE protein 1) (JSAPI) (Sunday driver 2).
 GN MAPK8IP3 OR JSAPI OR JIP3 OR SYD2.
 OC Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1A), FUNCTION, PHOSPHORYLATION, AND
 RP INTERACTION WITH MAPK8; MAPK9; MAPK10; MAPK14 AND MAPK1.
 RC TISSUE=Brain;
 RC MEDLINE=99455010; PubMed=10523642;
 RA Ito M., Yoshida K., Akechi M., Yamashita S., Takamatsu N.,
 RA Sugiyama K., Hibi M., Nakabeppu Y., Shiba T., Yamamoto K.-I.,
 RA "JSAPI, a novel Jun N-terminal protein kinase (JNK)-binding protein
 RT that functions as a scaffold factor in the JNK signaling pathway.";
 RT Mol. Cell. Biol. 19:7539-7548(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1A; 1B; 1C; 1D AND 1E), AND TISSUE
 RP SPECIFICITY.
 RC TISSUE=Brain;
 RC MEDLINE=20480689; PubMed=11024282;
 RA Ito M., Akechi M., Hirose R., Ichimura M., Takamatsu N., Xu P.,
 RA Nakabeppu Y., Tadaoishi S., Yamamoto K.-I., Yoshida K.,
 RT "Isoforms of JSAPI scaffold protein generated from alternative
 RT splicing.";
 RT Gene 255:229-234(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1C AND 3A), FUNCTION, INDUCTION, TISSUE
 RP SPECIFICITY, SUBCELLULAR LOCATION, PHOSPHORYLATION, MUTAGENESIS OF
 RP ARG-205; PRO-206; THR-207; SER-208; LEU-208; THR-206 AND THR-206 AND
 RP THR-287, AND INTERACTION WITH MAPK8IP2; MAPK8; MAPK9; MAPK10; MAPK17
 RP AND MAPK11.
 RC STRAIN=C57BL/6; TISSUE=Brain, and Heart;
 RC MEDLINE=20094982; PubMed=10629660;
 RA Kelkar N., Gupta S., Dickens M., Davis R.J.,
 RT "Interaction of a mitogen-activated protein kinase signaling module
 RT with the neuronal protein JIP3.";
 RT Mol. Cell. Biol. 20:1030-1043(2000).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1C), SUBCELLULAR LOCATION, AND INTERACTION
 RP WITH KLC1.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RC MEDLINE=20560743; PubMed=11106729;
 RA Bowman A.B., Kamal A., Ritchings B.W., Philp A.V., McGrail M.,
 RA Gindhart J.G., Goldstein L.S.B.,
 RT "Kinesin-dependent axonal transport is mediated by the Sunday Driver
 RT (SYD) protein.";
 RT Cell 103:583-594(2000).
 RN [5]
 RP SEQUENCE OF 1240-1337 FROM N.A.
 RP MEDLINE=22388257; PubMed=12477932;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hilyk S.W.,
 RA Dichtchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stedler M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantino P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield V.S.N., Krzywinski M.I., Skalski S., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP INTERACTION WITH KLC.
 RC TISSUE=Brain;
 RC MEDLINE=21135887; PubMed=11238452;
 RA Verhey K.J., Meyer D., Deehan R., Blenis J., Schnapp B.J.,
 RA Rapoport T.A., Margolis B.,
 RT "Cargo of kinesin identified as JIP scaffolding proteins and
 RT associated signaling molecules.";
 RT J. Cell Biol. 152:959-970(2001).
 RN [7]
 RP FUNCTION: The JNK-interacting protein (JIP) group of scaffold
 RP proteins selectively mediates JNK signaling by aggregating
 RP specific components of the MAPK cascade to form a functional JNK
 RP signaling module. May function as a regulator of vesicle
 RP transport, through interactions with the JNK-signaling components
 RP and motor proteins.
 CC [8]
 CC SUBUNIT: Forms homo- or heterooligomeric complexes. The central
 CC region of Mapk8ip3 interacts with the C-terminal of Mapk8ip2 but
 CC not Mapk8ip1. Binds specific components of the JNK signaling
 CC pathway namely Mapk8, Mapk9 and Mapk10 to the N-terminal region,
 CC Mapk24 and Mapk27 to the central region and Mapk11 to the C-
 CC terminal region. Binds the TPR motif-containing C-terminal of
 CC kinesin light chain, pre-assembled Mapk8ip1 scaffolding complexes
 CC are then transported as a cargo of kinesin, to the required
 CC subcellular location.
 CC [9]
 CC SUBCELLULAR LOCATION: Cytoplasmic; localised in the soma and
 CC growth cones of differentiated neurites and the Golgi and vesicles
 CC of the early secretory compartment of epithelial cells.
 CC [10]
 CC ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=6;
 CC Name=1c; Synonyms=3b;
 CC Name=1a;
 CC Name=1b;
 CC IsoId=Q9ESN9-2; Sequence=VSP_002775, VSP_002777;
 CC Name=1d;
 CC IsoId=Q9ESN9-3; Sequence=VSP_002776, VSP_002777;
 CC Name=1e;
 CC IsoId=Q9ESN9-4; Sequence=VSP_002775;
 CC Name=1f;
 CC IsoId=Q9ESN9-5; Sequence=VSP_002778, VSP_002779;
 CC Name=1g;
 CC IsoId=Q9ESN9-6; Sequence=VSP_002776;
 CC [11]
 CC TISSUE SPECIFICITY: Highly expressed throughout many regions of
 CC the brain and at lower levels in the heart, liver, lung, testes
 CC and kidney. All isoforms have been identified in the brain.
 CC Mapk8ip3a is also expressed in the spleen and lung.
 CC [12]
 CC INDUCTION: Expressed in neurites 5 days following initiation of
 CC nerve growth factor Ngf induced differentiation. Ngf withdrawal
 CC results in the down-regulation of Mapk8ip3 protein by caspase-
 CC mediated cleavage.
 CC [13]
 CC SIMILARITY: Belongs to the JIP scaffold family.
 CC [14]
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 CC [15]
 CC EMBL; AB005662; BAB85874.1; -
 CC EMBL; AB043124; BAB16675.1; -
 CC EMBL; AB043125; BAB16676.1; -
 CC EMBL; AB043129; BAB16684.1; -
 CC EMBL; AB043129; BAB16685.1; -
 CC EMBL; AB043126; BAB16685.1; JOINED.
 CC EMBL; AB043127; BAB16685.1; JOINED.
 CC EMBL; AB043128; BAB16685.1; JOINED.
 CC EMBL; AF178637; AAF26843.1; -
 CC EMBL; AF178637; AAF26843.1; -
 CC EMBL; AF262046; AAG36931.1; ALT_INT.
 CC EMBL; BC004003; AA040003.1; -

[illegible]

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Katayama S., Dai H., Arellano M., Perez P., Toda T.;
RT "Fission yeast alpha-glucan synthase Moki localizes closely with actin
RL function." ;
RM Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11659360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Seguros K., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor A., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean U.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymmonet B.,
RA Wellens I., Vanstreels E., Risger M., Schaefer M., Wempeier B.,
RA Gabell C., Fuchs M., Fritz C., Holzner E., Meesal D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Wandt R., Purcell B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leteune V., Motlier S.,
RA Calbert F., Aves S.J., Xiang Z., Hunt C., Moore X., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garçon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Usero D., Barrett B.G., Nurse P.;
RL "The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
CC -I- CANDLYTIC ACTIVITY: UDP-glucose + {alpha-D-glucosyl-(1,3)}(N) =
CC UDP + {alpha-D-glucosyl-(1,3)}(N+1).
CC -I- SIMILARITY: Belongs to the glycosyltransferase family 1.
CC -----
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CC -----
CC EMBL: AB018383; BAA76550.1; -
DR EMBL: AL049522; CAB40008.1; -
DR PIR: TA3433; TA3433
DR GeneDB: Spombe, SPCC63.04; -
DR InterPro: IPR001296; Glyco_transf_1.
DR Pfam: PF00534; Glycos_transf_1; 1.
KW Cell wall; Transferase; Glycosyltransferase.
SQ SEQUENCE 1369 AA; 156161 MW; AOB0DMA357EBB8BE9A CRC64;

Query March 56.2%; Score 36; DB 1; Length 1369;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

      1 WDEPLTKLM 9
      |||||
Db    1183 WGSKLTGLM 1191

RESULT 59
YF70_META STANDARD; PRT; 115 AA.
ID YF70_META
CD OS8965;
```

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DT Hypothetical protein MJ1570.
 GN MJ1570.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 CC Methanocaldococcaceae; Methanocaldococcus.
 NCBI_TaxID=2190;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=9633799; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerecavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Frazer C.M., Smith H.O., Moese C.R., Venter J.C.,
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: TO M.THERMOPHILICUM MTH1706.
 CC -----
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 CC -----
 CC EMBL; U67597; AAB9594.1; -.
 DR PIR; A64496; A64496.
 DR TIGR; MJ1570; -.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 11 31 POTENTIAL.
 FT TRANSMEM 85 105
 SQ SEQUENCE 115 AA; 12632 MW; 7DEA6DE6131C6A8 CRC64;
 QY Query Match 54.7%; Score 35; DB 1; Length 115;
 Best Local Similarity 60.0%; Pred. No. 38;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Db 1 WYDPLTKML 10
 3 WQDPLVKKFL 12
 RESULT 60
 RNHL_HUMAN STANDARD; PRT; 299 AA.
 AC 075792; 096F11;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ribonuclease HI large subunit (EC 3.1.26.-) (RNase HI large subunit)
 DE (RNase H(35)) (Ribonuclease H2) (RNase H2).
 GN RNASBH2A OR RNASBHI OR RNH1A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=99007233; PubMed=9789007;
 RA Frank P., Braunhofer-Reiter C., Wintereberger U., Grimm R.,
 RA Buesen W.;
 RT "Cloning of the cDNA encoding the large subunit of human RNase HI, a
 RT homologue of the prokaryotic RNase HI.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:12872-12877(1998).

RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strauberg R.L., Feinberg E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditschenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshitsugu S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bock S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalek U., Smalins D.E.,
 RA Scherch A., Schein J.B., Jones S.U.M., Maiz M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Degrades the ribonucleotide moiety on RNA-DNA hybrid
 CC molecules. Participates in DNA replication.
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
 CC phosphomonoester.
 CC -1- SIMILARITY: Belongs to the RNase HII family. Eukaryotic subfamily.
 CC -----
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 CC -----
 CC EMBL; Z97029; CAB09725.1; -.
 DR EMBL; BC011748; AAH11748.1; -.
 DR HSSP; Q57599; 1EKE.
 DR Genew; HGNC:18518; RNASBH2A.
 DR MIM; 606034; -.
 DR GO; GO:0004540; P:ribonuclease activity; TAS.
 DR GO; GO:0006260; P:DNA replication; TAS.
 DR GO; GO:0006401; P:RNA catabolism; TAS.
 DR InterPro; IPR001352; RNase HII/HIII.
 DR InterPro; IPR004649; RhlH.
 DR Pfam; PF01351; RNase_HII; 1.
 DR TIGRFAMs; TIGR00729; TIGR00729; 1.
 KW Hydrolyase; Nuclease; Endonuclease.
 FT ACT_SITE 34 34
 FT ACT_SITE 141 141 BY SIMILARITY.
 FT ACT_SITE 169 169 BY SIMILARITY.
 FT CONFLICT 152 152 R->O (IN REF. 1).
 SQ SEQUENCE 299 AA; 33395 MW; 34992F8B5130157B CRC64;
 QY Query Match 54.7%; Score 35; DB 1; Length 299;
 Best Local Similarity 75.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 3 DPLTKML 10
 213 DPKTKWL 220;
 RESULT 61
 RNHL_MOUSE STANDARD; PRT; 301 AA.
 AC 09CW18;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)

```

DE Ribonuclease HI large subunit (EC 3.1.26.-) (RNase HI large subunit).
GN RNASEH2A OR RNASEH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner T., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glass C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakado T., Pesole G., Quackenbush J.,
RA Schiml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: Degrades the ribonucleotide moiety on RNA-DNA hybrid
CC molecules. Participates in DNA replication (By similarity).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphonucleoside.
CC -1- SIMILARITY: Belongs to the RNase HII family. Eukaryotic subfamily.
CC
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CC
CC EMBL: AK010292; BAB26828.1; -.
CC DR HSSP: O57599; 1EXE.
CC DR MGD: MG1:1916974; 2400006P09R1K.
CC DR InterPro: IPR001352; RNase_HII/HIII.
CC DR InterPro: IPR004649; Rnh1I.
CC DR Pfam: PF01351; RNase_HII.1.
CC DR TIGRPFAMs: TIGR00729; TIGR00729.1.
CC DR HydroLase; Nuclease; Endonuclease.
CC FT ACT SITE 34 34 BY SIMILARITY.
CC FT ACT SITE 142 142 BY SIMILARITY.
CC FT ACT SITE 170 170 BY SIMILARITY.
CC SQ SEQUENCE 301 AA; 33541 MW; ADF92D23F1DB43BF CRC64;

Query Match 54.7%; Score 35; DB 1; Length 301;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 3 DPLTKML 10
DB 214 DPKTKML 221

```

RESULT 62
PBN2 ANASP STANDARD; PRT; 306 AA.
AC Q82074;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

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DE Probable inorganic polyphosphate/ATP-NAD kinase 2 (EC 2.7.1.23)
GN PPNK2 OR ATP NAD kinase 2).
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21595285; PubMed=11759840;
RX Kameko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriuchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.,
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
CC -1- FUNCTION: Catalyzes the phosphorylation of NAD to NADP. Utilizes
CC ATP and other nucleoside triphosphates as well as inorganic
CC polyphosphate as a source of phosphorus (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + NAD(+) = ADP + NADP(+).
CC -1- COFACTOR: Divalent metal ions (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the NAD kinase family.
CC
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CC
CC EMBL: AP003581; BAB77751.1; -.
CC DR PIR: A1835; A1835.
CC DR HAMAP: MF_00361; -1.
CC DR InterPro: IPR002564; ATP_NADK.
CC DR Pfam: PF01513; NAD_Kinase.1.
CC KW "transferase; kinase; NAD; NADP; Complete proteome.
CC SQ SEQUENCE 306 AA; 33933 MW; 92FF532C5F3D15A6 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 306;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 2 YDPLTKML 10
DB 241 YDLSTKML 249

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RESULT 63
YPOR ACICA STANDARD; PRT; 315 AA.
AC P07783;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in PQO-III 3' region (ORF R) (Fragment).
OS Acinetobacter calcoaceticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LMD 79.41;
RX MEDLINE=89123056; PubMed=2536663;
RA Goosen N., Horsman H.P.A., Huinen R.G.M., van de Putte P.,
RT "Acinetobacter calcoaceticus genes involved in biosynthesis of the
RT coenzyme pyridoxal-quinoline-quinone: nucleotide sequence and
RT expression in Escherichia coli K-12.";
RL J. Bacteriol. 171:447-455(1989).
CC -1- FUNCTION: Not known.
CC -1- SIMILARITY: TO AN ORF IN THE 5' REGION OF PQOA IN K. PNEUMONIAE.

```

CC -1- SIMILARITY: Belongs to peptidase family M19.
CC -----
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CC -----
CC EMBL; X06452; CAA29758.1; -
CC DR MEROPS; M19.003; -
CC DR InterPro; IPR000180; Pept_M19_AS.
CC DR InterPro; IPR008257; Peptidase_M19.
CC DR Pfam; PF01244; Renal_dipeptidase; 1.
CC DR PROSITE; PS00869; RENAL_DIPEPTIDASE; 1.
CC DR Hypothetical protein.
CC KW NON TER 315 315
CC FT
CC SQ SEQUENCE 315 AA; 35597 MW; 6F2EC2B6F4D5FB7B CRC64;

Query Match 54.7%; Score 35; DB 1; Length 315;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 DPLTKLWL 10
DB 14 DALTRLWL 21

RESULT 64
Y493_MYCTU STANDARD; PRT; 329 AA.
ID Y493_MYCTU
AC Q11158;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein RV0493c/MT0513.
GN RV0493c OR MT0513 OR MTCY20G9.19C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=96295987; PubMed=9634220;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigemeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jørgensen K., Krogh A., McLaren J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sultston J.E., Taylor K., Whitehead S., Barrall B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M., Hatt D., Hickey B.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL J. Bacteriol. 184:5479-5490 (2002).
CC -1- SIMILARITY: SOME. TO M.LEPPAE B2168.F2.93.
CC -----
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CC -----
CC EMBL; Z77162; CAB00954.1; -
CC DR EMBL; AE006952; AAK44736.1; -
CC DR PIR; H70744; H70744.
CC DR TIGR; MT0513; -
CC DR Tubercultis; RV0493c; -
CC KW Hypothetical protein; Complete proteome.
CC SQ SEQUENCE 329 AA; 35427 MW; BE4B524750277B56 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 329;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 0; Indels 6; Gaps 2;

OY 1 WY----DPLTK--LWL 10
DB 36 WYATSDPLTKRLMV 51

RESULT 65
TPSB_CABEL STANDARD; PRT; 359 AA.
ID TPSB_CABEL
AC Q20351;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Putative protein-tyrosine sulfotransferase (EC 2.8.2.20)
DE (Tyrosyl)protein sulfotransferase (TPST).
GN F42G9.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodieridae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Tatch A.;
RT Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Catalyzes the O-sulfation of tyrosine residues within
CC acidic motifs of polypeptides (By similarity).
CC -1- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + protein tyrosine =
CC adenosine 3',5'-bisphosphate + protein tyrosine-O-sulfate.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By
CC similarity).
CC -1- SIMILARITY: Belongs to the protein sulfotransferase family.
CC -----
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CC -----
CC EMBL; U00051; AAA91354.1; -
CC DR PIR; T16350; T16350.
CC DR WormPep; F42G9.8; CE07235.
CC DR InterPro; IPR000863; Sulfotransferase.
CC DR Pfam; PF00685; Sulfotransfer; 1.
CC KW Hypothetical protein; Transferrase; Transmembrane; Glycoprotein;
CC KW Signal-anchor.
CC FT DOMAIN 1 27 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 28 48 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT
CC FT
CC SQ SEQUENCE 359 AA; 41469 MW; 9FC2F44539B8CC53 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 359;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 0; Indels 6; Gaps 2;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DPLTKML 10
DB 171 DPLTKML 178

RESULT 66

PYRC_THEMA STANDARD; PRT; 376 AA.

AC 09WYH0; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 15-MAR-2004 (Rel. 43, Last annotation update)

OS PyRC OR TM0335.

OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.

NCBI_TaxID=2336;

RP STRAIN=MSB / DSM 3109 / ATCC 43589;

RX MEDLINE=99287316; PubMed=10360571;

RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

RA Hatt D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

RA McDonald L., Ueteyback T.R., Malek J.A., Linher K.D., Garrett M.M.,

RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

RT "Evidence for lateral gene transfer between Archaea and Bacteria from

RT genome sequence of Thermotoga maritima."

RL Nature 399:323-329 (1999).

CC -1- CATALYTIC ACTIVITY: (S)-dihydroxycitrate + H(2)O = N-carbamoyl-L-

CC aspartate.

CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).

CC -1- PATHWAY: Pyrimidine biosynthesis; third step.

CC -1- SUBUNIT: Homodimer (By similarity).

CC -1- SIMILARITY: Belongs to the DHase family. Subfamily 2.

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CC EMBL; A001714; AAD35422.1; -

DR TIGR: TM0335; -

DR HAMAP; MF_00220; -; 1.

DR InterPro; IPR002195; Pept_M38_nph.

DR PROSITE; PS00482; DIHYDROXYROTAASE_1; 1.

DR PROSITE; PS00483; DIHYDROXYROTAASE_2; FALSE NEG.

KW Pyrimidine biosynthesis; Hydrolase; Metal-binding; Zinc;

KW Complete proteome.

FT METAL 35 35 ZINC 1 (BY SIMILARITY).

FT METAL 37 37 ZINC 1 (BY SIMILARITY).

FT METAL 138 138 ZINC 2 (BY SIMILARITY).

FT METAL 187 187 ZINC 2 (BY SIMILARITY).

FT METAL 257 257 ZINC 1 (BY SIMILARITY).

FT DOMAIN 128 132 POLY-TLS.

SQ SEQUENCE 376 AA; 4263 MW; C6SEDFEER0A95A81 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 376;

Best Local Similarity 55.6%; Pred. No. 1.3e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YDPLTKML 10

DB 4 YDPRKMT 12

RESULT 67

ASSY_OCEIH STANDARD; PRT; 417 AA.

AC 08ET8; 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DE Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartate

DE ligase).

GN ARG3 OR OR3129.

OS Oceanobacillus iheyensis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.

NCBI_TaxID=182710;

RP STRAIN=HTE831 / DSM 14371 / JCM 11309;

RX MEDLINE=2220767; PubMed=42253376;

RA Takami H., Takaki Y., Uchiyama I.,

RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya

RT Ridge and its unexpected adaptive capabilities to extreme

RT environments."

RL Nucleic Acids Res. 30:3927-3935(2002).

CC -1- CATALYTIC ACTIVITY: ATP + L-citrulline + L-aspartate = AMP +

CC dihydroxy-L-argininosuccinate.

CC -1- PATHWAY: Arginine biosynthesis; seventh step.

CC -1- SUBUNIT: Homotetramer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

CC -1- SIMILARITY: Belongs to the argininosuccinate synthase family.

CC Subfamily 1.

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CC EMBL; AP004603; BAC15085.1; -

DR HAMAP; MF_00005; -; 1.

DR InterPro; IPR001518; Arginosec synth.

DR Pfam; PF00764; Arginosec synth; 1.

DR ProDom; PD003544; Arginosec synth; 1.

DR TIGRFAMs; TIGR00032; argG; 1

DR PROSITE; PS00564; ARGINOSUCCIN SYN_1; 1.

DR PROSITE; PS00565; ARGINOSUCCIN SYN_2; 1.

KW Arginine biosynthesis; ligase; ATP-binding; Complete proteome.

SQ SEQUENCE 417 AA; 46068 MW; E9A53AD374AD7CA2 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 417;

Best Local Similarity 71.4%; Pred. No. 1.4e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTK 7

DB 316 WYSPLE 322

RESULT 68

ER24_SCHPO STANDARD; PRT; 424 AA.

AC 009195; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Delta(14)-sterol reductase (EC 1.3.1.70) (C-14 sterol reductase)

DE (Sterol C14-reductase).

GN ERG24 OR SPBC16G5.18.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

NCBI_TaxID=4896;


```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=SP66;
RX  MEDLINE=95212923; PubMed=7698661;
RT  RA Smith S.;
RT  "Cloning and sequence analysis of an ERG24 homolog from
RT  Schizosaccharomyces pombe.";
RT  Gene 155:139-140(1995).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=972;
RX  MEDLINE=21848401; PubMed=11859360;
RA  Wood V., Gilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA  Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA  Collins M., Connor R., Cronin A., Davis P., Fellwell T., Frazer A.,
RA  Gentile S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA  Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagele K.,
RA  James K., Jones L., Jones M., Leather S., McDonald S., Mclean J.,
RA  Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA  Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA  Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA  Skelton J., Slatmonde M., Squares R., Stevens K.,
RA  Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA  Woodward J., Volckaert G., Aert R., Robben J., Gymnopoulos B.,
RA  Welfjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA  Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA  Borzym K., Langer I., Beck A., Leinrich R., Reinhardt R., Pohl T.M.,
RA  Eger P., Zimmermann W., Medler H., Wambutt R., Purrelle B.,
RA  Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motlier S.,
RA  Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA  Lucas M., Rochet M., Gallardin C., Tallada V.A., Garçon A., Thode G.,
RA  Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA  Dominguez L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA  Cerutti L., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA  Shpakovski G.V., Useery D., Barrell B.G., Nurse P.;
RT  "The genome sequence of Schizosaccharomyces pombe.";
RL  Nature 415:871-880(2002).
CC  -1- FUNCTION: REDUCES THE C14=C15 DOUBLE BOND OF 4,4-DIMETHYL-
CC  CHOLESTA-8,14,24-TRIENOL TO PRODUCE 4,4-DIMETHYL-CHOLESTA-8,24-
CC  DIENOL (BY SIMILARITY).
CC  -1- CATALYTIC ACTIVITY: 4,4-dimethyl-5-alpha-cholesta-8,24-dien-3-
CC  beta-ol + NADP(+) = 4,4-dimethyl-5-alpha-cholesta-8,14,24-trien-3-
CC  beta-ol + NADPH.
CC  -1- PATHWAY: Ergosterol biosynthesis.
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC  -1- SIMILARITY: Belongs to the ERG4/ERG24 family.
CC  -----
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CC  -----
DR  EMBL, U36039; AAA74121.1; -.
DR  EMBL, AL023554; CA019037.1; -.
DR  PIR, JC4057; JC4057.
DR  GenBank, SPBC16G5.18; -.
DR  InterPro, IPR001171; ERG4 ERG24.
DR  Pfam, PF01222; ERG4_ERG24_1.
DR  PROSITE, PS01017; STEROL_REDUCT_1; 1.
DR  PROSITE, PS01018; STEROL_REDUCT_2; 1.
KW  Sterol biosynthesis; Oxidoreductase; NADP; Transmembrane.
FT  TRANSMEM 19 39
FT  TRANSMEM 112 132
FT  TRANSMEM 370 390
FT  TRANSMEM 424 AA; 48560 MM; 1DCE704F1E5F5B CRC64;
SQ  SEQUENCE

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Query Match          54.7% Score 35; DB 1; Length 424;
Best Local Similarity 55.6% Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY  1 WYDPLTKW 9
DB  72 WFTLTLLW 80
RESUL 69
MK08 XENLA STANDARD; PRT; 426 AA.
ID  MK08 XENLA
AC  Q8QHK8; Q8JJC3;
DT  10-OCT-2003 (Rel. 42, Created)
DT  10-OCT-2003 (Rel. 42, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Mitogen-activated protein kinase 8 (EC 2.7.1.37) (Stress-activated
DE  protein kinase JNK1).
GN  JNK1.
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8395;
RN  [1]
RP  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, COFACTOR, TISSUE
RP  SPECIFICITY, AND ENZYME REGULATION.
RC  TISSUE=Oocyte;
RX  MEDLINE=21657088; PubMed=11751577;
RA  Yamada H., Moriguchi T., Masuyama N., Kusakabe M., Hanafusa H.,
RA  Takada R., Takada S., Nishida E.;
RT  "JNK functions in the non-canonical Wnt pathway to regulate convergent
RT  extension movements in vertebrates.";
RL  EMBO Rep. 3:69-75(2002).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Embryo;
RA  Klein S., Strausberg R.;
RL  Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC  -1- FUNCTION: Responds to activation by environmental stress and pro-
CC  inflammatory cytokines by phosphorylating a number of
CC  transcription factors, and thus regulating transcriptional
CC  activity (By similarity). Regulates morphogenic cell movements,
CC  controlling convergent extension during gastrulation.
CC  -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC  -1- COFACTOR: Magnesium.
CC  -1- ENZYME REGULATION: Activated by threonine and tyrosine
CC  phosphorylation, potentially by the dual-specificity kinase, MKK7.
CC  Indirectly activated by Wnt5a.
CC  -1- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=2;
CC  Name=1; Synonym=Alpha;
CC  IsoId=Q8QHK8-1; Sequence=Displayed;
CC  Name=2; Synonym=Beta;
CC  IsoId=Q8QHK8-2; Sequence=VSP_007348, VSP_007349;
CC  -1- TISSUE SPECIFICITY: Strongly expressed in presumptive ectoderm and
CC  mesoderm regions and weakly expressed in endoderm regions during
CC  dorsal stages of embryo development. Expressed in the head and
CC  dorsal regions during neurula and tailbud stages.
CC  -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. MAP
CC  kinase subfamily.
CC  -----
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CC  -----
DR  EMBL, AB073999; BAB85483.1; -.
DR  EMBL, AB074000; BAB81458.1; -.
DR  EMBL, BC046834; AAH46834.1; -.
DR  HSSP; P24941; 1BUH.
DR  GO; GO:0005634; C:nucleus; ISS.
DR  GO; GO:0004705; F:JUN kinase activity; ISS.

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DR GO; GO:0009795; P:embryonic morphogenesis; IDA.
 DR GO; GO:0007254; P:JNK cascade; ISS.
 DR InterPro; IPR008351; JNK MAPK.
 DR InterPro; IPR003527; MAP_kin.
 DR InterPro; IPR000719; Src_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase.1.
 DR PRINTS; PR01772; JNKMAPKINASE.
 DR ProDom; PD000001; Prot_kinase.1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS01351; MAPK.1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
 DR PROSITE; PS00101; PROTEIN KINASE DOM.1.
 DR PROSITE; PS00108; PROTEIN KINASE_ST.1.
 DR ATP-binding; Transferase; Serine/threonine-protein kinase;
 KW Phosphorylation; Developmental protein; Alternative splicing.
 FT DOMAIN 26 321
 FT NP_BIND 33 38
 FT BINDING 55 55
 FT ACT_SITE 151 151
 FT MOD_RES 183 183
 FT MOD_RES 185 185
 FT VARSPPLIC 380 384
 FT VARSPPLIC 385 426
 FT SEQUENCE 426 AA; 47928 MW; 51990EC50A556092 CRC64;
 Query Match 54.7%; Score 35; DB 1; Length 426;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WYDPL 5
 Db 324 WYDPL 328

RESULT 70
 FTSM MYCLE STANDARD; PRT; 465 AA.
 AC 050186;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable cell division protein ftsw.
 GN FTSM OR RODA OR ML0019.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_Taxid=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fstli H., Salazar L., Takiff H.E., Cole S.T.;
 RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Elgimeier K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Basham D., Brown D., Chillingworth T., Harris D.,
 RA Davies R.M., Devlin K., Duthoy S., Felwell T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagsels K., Lacroix C., Maclean J., Moule S.,
 RA Rutter S., Seeger K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Squares S., Stevens K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Barrell B.G.;
 "Massive gene decay in the leprosy bacillus."

RL Nature 409:1007-1011(2001).
 CC -!- FUNCTION: This is a septum-peptidoglycan biosynthetic protein,
 CC involved in cell wall formation. Plays a role in the stabilization
 CC of the ftsz ring during cell division (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE FTSW/RODA/SPOVE FAMILY.
 CC -----
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 CC -----
 DR EMBL; Z70722; CA94715.1; -.
 DR EMBL; AL583917; CAC9527.1; -.
 DR PIR; C86911; C86911.
 DR PIR; T10012; T10012.
 DR Leproma; ML0019; -.
 DR InterPro; IPR001182; Cell cycle.
 DR Pfam; PF01098; FTSW RODA SPOVE.1.
 DR PROSITE; PS00428; FTSW RODA SPOVE.1.
 KW Peptidoglycan synthesis; Cell wall; Cell division; Cell shape;
 KW Transmembrane; Complete proteome.
 FT TRANSMEM 22 42
 FT TRANSMEM 50 70
 FT TRANSMEM 76 96
 FT TRANSMEM 115 135
 FT TRANSMEM 144 164
 FT TRANSMEM 179 199
 FT TRANSMEM 222 242
 FT TRANSMEM 243 263
 FT TRANSMEM 264 284
 FT TRANSMEM 308 328
 FT TRANSMEM 340 360
 FT TRANSMEM 382 402
 FT TRANSMEM 414 434
 FT TRANSMEM 419 434
 FT CONFLICT 319 320
 FT SEQUENCE 465 AA; 50468 MW; CA656039538EBC24 CRC64;
 Query Match 54.7%; Score 35; DB 1; Length 465;
 Best Local Similarity 62.5%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 WYDPLTKL 8
 Db 294 WYDPLTKL 301

RESULT 71
 BGAL SULSH STANDARD; PRT; 489 AA.
 AC P50388;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Beta-galactosidase (EC 3.2.1.23) (Lactase).
 GN BGLY.
 OS Sulfolobus shibatae.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_Taxid=2286;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 51178 / DSM 5389 / B12;
 RA Comaritis H., Charalambous B.M.;
 RT "The development and application of genetical techniques for the
 RT extremely thermocophilic archaeon Sulfolobus shibatae."
 RL Submitted (Oct-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-
 CC galactose residues in beta-D-galactosides.
 CC -!- SUBUNIT: Homotetramer.

CC -1- SIMILARITY: Belongs to family 1 of glycosyl hydrolases.
CC -----
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CC -----
DR EMBL; L47841; AAA79030.1; -.
DR HSSP; P22498; 1GOW.
DR InterPro: IPR001360; Glyco_hydro_1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR ProDom; PD000650; Glyco_hydro_1; 1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
KW Hydrolase; Glycosidase.
FT ACT_SITE 206 206 PROTON DONOR (POTENTIAL).
FT ACT_SITE 387 387 NUCLEOPHILE (BY SIMILARITY).
SQ SEQUENCE 489 AA; 56564 MW; 32412888F478842B CRC64;
Query Match 54.7%; Score 35; DB 1; Length 489;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 YDPLTKMW 9
DB 369 YDVLTKYW 376
RESULT 72
EGAL_SULSO STANDARD; PRT; 489 AA.
ID _BGAL_SULSO
AC P22498; Q9V2Z5;
DT 01-AUG-1991 (Rel. 19, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-galactosidase (EC 3.2.1.23) (Lactase).
GN LACS OR SSO3019.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-33.
RC STRAIN=ATCC 49255 / DSM 5833 / MT-4;
RX MEDLINE=91033070; PubMed=2121622;
RA Cubellis M.V., Rozzo C., Montecuchi P., Rossi M.,
RT "Isolation and sequencing of a new beta-galactosidase-encoding
RL archaeobacterial gene.";
RL Gene 94:89-94(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=98/2;
RX MEDLINE=99315783; PubMed=10383958;
RA Haebelstine C., Montalvo-Rodriguez R., Bini E., Carl A., Blum P.,
RT "Coordinate transcriptional control in the hyperthermophilic archaeon
RL Sulfolobus solfataricus.";
RL J. Bacteriol. 181:3920-3927(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Aweyer M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moers A., Erasmo G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.,
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RC STRAIN=ATCC 49255 / DSM 5833 / MT-4;
RX MEDLINE=97446327; PubMed=9299327;
RA Aguilar C.F., Sanderson I., Moracci M., Ciaramella M., Nucci R.,
RA Rossi M., Pearl L.H.;
RT "Crystal structure of the beta-glycosidase from the hyperthermophilic
RT archaeon Sulfolobus solfataricus: resilience as a key factor in
RT thermostability.";
RL J. Mol. Biol. 271:789-802(1997).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-
CC galactose residues in beta-D-galactosides.
CC -1- SUBUNIT: Homotetramer.
CC -1- SIMILARITY: Belongs to family 1 of glycosyl hydrolases.
CC -----
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CC -----
DR EMBL; M34696; AAA72843.1; -.
DR EMBL; AF133036; AAD21094.1; -.
DR EMBL; AE006893; AAK43121.1; -.
DR PIR; B90483; B90483.
DR PIR; JQ0767; JQ0767.
DR PDB; 1GOW; 20-AUG-97.
DR InterPro: IPR001360; Glyco_hydro_1.
DR Pfam; PF00232; Glyco_hydro_1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR ProDom; PD000650; Glyco_hydro_1; 1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
KW Hydrolase; Glycosidase; 3D-structure; Complete proteome.
FT ACT_SITE 206 206 PROTON DONOR (POTENTIAL).
FT ACT_SITE 387 387 NUCLEOPHILE (BY SIMILARITY).
FT CONFLICT 235 235 A -> H (IN REF. 1).
FT STRAND 2 3
FT TURN 6 7
FT STRAND 9 13
FT HELIX 16 19
FT TURN 21 22
FT TURN 24 25
FT STRAND 31 31
FT HELIX 32 36
FT TURN 37 38
FT HELIX 40 44
FT TURN 45 46
FT HELIX 53 55
FT TURN 59 61
FT HELIX 63 72
FT TURN 73 74
FT STRAND 77 81
FT HELIX 84 87
FT TURN 100 101
FT HELIX 112 118
FT TURN 119 121
FT HELIX 124 140
FT TURN 141 141
FT STRAND 143 149
FT STRAND 154 154
FT HELIX 155 157
FT STRAND 158 158
FT HELIX 160 164
FT TURN 165 166
FT STRAND 172 172
FT HELIX 173 175
FT HELIX 177 194
FT TURN 195 197
FT STRAND 200 205

FT HELIX 207 215
 FT TURN 216 216
 FT HELIX 218 220
 FT HELIX 220 220
 FT HELIX 229 253
 FT STRAND 258 269
 FT HELIX 272 274
 FT HELIX 275 285
 FT TURN 286 286
 FT HELIX 287 295
 FT STRAND 297 302
 FT TURN 301 302
 FT STRAND 303 306
 FT TURN 308 312
 FT STRAND 317 330
 FT TURN 331 332
 FT STRAND 333 336
 FT TURN 341 342
 FT STRAND 346 347
 FT TURN 349 352
 FT TURN 351 352
 FT STRAND 355 356
 FT TURN 358 359
 FT STRAND 362 362
 FT TURN 365 365
 FT HELIX 366 379
 FT STRAND 383 387
 FT HELIX 398 414
 FT TURN 415 416
 FT STRAND 419 425
 FT STRAND 428 428
 FT HELIX 433 438
 FT STRAND 444 447
 FT TURN 448 451
 FT STRAND 452 455
 FT HELIX 457 466
 FT TURN 467 469
 FT STRAND 470 471
 FT HELIX 473 475
 FT TURN 476 477
 FT TURN 485 486
 SO SEQUENCE 489 AA; 56691 MW; B56F6CE8E8E4A429D CRC64;

Query Match 54.7%; Score 35; DB 1; Length 489;
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKW 9
 Db 369 YDPLTKW 376

RESULT 73
 BACE_HUMAN STANDARD; PRT; 501 AA.
 ID P56817; Q9BYB9; Q9BYC0; Q9BYC1; Q9UJ75;
 AC 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DB Beta-secretase precursor (BC 3.4.23.46) (Beta-site APP cleaving enzyme) (beta-site amyloid precursor protein cleaving enzyme) (Aspartyl protease 2) (Asp 2) (ASPP2) (Membrane-associated aspartic protease 2) (Memapsin-2).
 DE BACE OR BACE1.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC TISSUE=Brain;
 RX MEDLINE=20002972; PubMed=10531052;
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A., Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,

RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J., Rogers G., Cilton M.,
 RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by the transmembrane aspartic protease BACE.",
 RL Science 286:735-741(1999).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORM A), SEQUENCE OF 46-68, AND
 RP CHARACTERIZATION.
 RC TISSUE=Brain;
 RX MEDLINE=20057171; PubMed=10591214;
 RA Sima S., Anderson J.P., Barbour R., Basi G.S., Caccavello R.,
 RA Davis D., Doan M., Dovey H.F., Frigon N., Hong J., Jacobson-Croak K.,
 RA Jewett N., Keim P., Knops J., Lieberburg I., Power M., Tan H.,
 RA Tatsuno G., Tung J., Schenk D., Seubert P., Suemasa S.M., Wang S.,
 RA Walker D., Zhao J., McConlogue L., Varghese J.,
 RT "Purification and cloning of amyloid precursor protein beta-secretase from human brain.",
 RL Nature 402:537-540(1999).
 [3]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=20057170; PubMed=10591213;
 RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
 RA Braslier J.R., Strachan N.C., Mathews W.R., Buhl A.E., Carter D.B.,
 RA Tomaseelli A.G., Parodi L.A., Heinrikson R.L., Gurey M.E.,
 RT "Membrane-anchored aspartyl protease with Alzheimer's disease beta-secretase activity.",
 RL Nature 402:533-537(1999).
 [4]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=20120043; PubMed=10656250;
 RA Hussain I., Powell D.V., Howlett D.R., Tew D.G., Meek T.D.,
 RA Chapman C., Glover I.S., Murphy K.E., Southan C.D., Ryan D.M.,
 RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.,
 RT "Identification of a novel aspartic proteinase (Asp 2) as beta-secretase.",
 RL Mol. Cell. Neurosci. 14:419-427(1999).
 [5]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RC TISSUE=Brain, and Pancreas;
 RA Zaccchetti D., De Pietri Tonelli D., Zaccchetti D., Keller P.,
 RT "New beta-site APP cleaving enzyme isoform (BACE-1B) obtained from human brain and pancreas.",
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 [6]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RC TISSUE=Pancreas;
 RA Zaccchetti D., De Pietri Tonelli D., Schnurbus R.,
 RT "New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from human pancreas.",
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 [7]
 RP SEQUENCE FROM N.A. (ISOFORMS B, C AND D).
 RC TISSUE=Brain;
 RX MEDLINE=21408467; PubMed=11516562;
 RA Tanahashi H., Tabira T.,
 RT "Three novel alternatively spliced isoforms of the human beta-site amyloid precursor protein cleaving enzyme (BACE) and their effect on amyloid beta-peptide production.",
 RL Neurosci. Lett. 307:9-12(2001).
 [8]
 RP SEQUENCE OF 14-501 FROM N.A. (ISOFORM A), AND CHARACTERIZATION.
 RX MEDLINE=20144060; PubMed=10677483;
 RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.,
 RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of beta-amyloid precursor protein.",
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
 [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=21950860; PubMed=11953458;
 RA Fischer F., Molinari M., Bodendorf U., Paganetti P.,
 RT "The disulphide bonds in the catalytic domain of BACE are critical but not essential for amyloid precursor protein processing activity.",

CC J. Neurochem. 80:1079-1088(2002).
 CC -1- FUNCTION: Responsible for the proteolytic processing of the
 CC amyloid precursor protein (APP). Cleaves at the amino terminus of
 CC the A-beta peptide sequence, between residues 671 and 672 of APP,
 CC leads to the generation and extracellular release of beta-cleaved
 CC soluble APP, and a corresponding cell-associated carboxy-terminal
 CC fragment which is later release by gamma-secretase.
 CC -1- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
 CC Val-Aen-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
 CC Alzheimer's amyloid precursor protein.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=A; Synonyms=BACE-1A, BAC-501;
 CC IsoId=P56817-1; Sequence=Displayed;
 CC Name=B; Synonyms=BACE-1B, BACE-1-476;
 CC IsoId=P56817-2; Sequence=VSP_005223;
 CC Name=C; Synonyms=BACE-1C, BACE-1-457;
 CC IsoId=P56817-3; Sequence=VSP_005222;
 CC Name=D; Synonyms=BACE-1D, BACE-1-432;
 CC IsoId=P56817-4; Sequence=VSP_005222, VSP_005223;
 CC -1- TISSUE SPECIFICITY: Brain.
 CC -1- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC -----
 CC EMBL; AF190725; AAF04142.1; -
 CC EMBL; AF201468; AAF18982.1; -
 CC EMBL; AF200343; AAF17079.1; -
 CC EMBL; AF204943; AAF26367.1; -
 CC EMBL; AF338816; AAK38374.1; -
 CC EMBL; AF338817; AAK38375.1; -
 CC EMBL; AB050436; BAB40931.1; -
 CC EMBL; AB050437; BAB40932.1; -
 CC EMBL; AB050438; BAB40933.1; -
 CC EMBL; AF200193; AAF13715.1; -
 CC PIR; A59090; A59090.
 CC PIR; A59090; A59090.
 CC PDB; 1MAH; 28-AUG-02.
 CC MEROPS; A01.004; -
 CC GeneW; HGNC:933; BACE.
 CC MIM; 604252; -
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0008798; F:beta-aspartyl-peptidase activity; TAS.
 CC GO; GO:0009405; P:pathogenesis; TAS.
 CC GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
 CC InterPro; IPR001969; Asparticase_AS.
 CC InterPro; IPR009007; Pept_A acid.
 CC InterPro; IPR001461; Peptidase_A1.
 CC Pfam; PF00026; asp; 1.
 CC PRINTS; PR00792; PEPsin.
 CC PROSITE; PS00141; ASP_PROTEASE; 1.
 CC HydroLase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 CC Signal; Alternative splicing; 3D-structure.
 CC SIGNAL 1 21
 CC PROPEP 22 45
 CC CHAIN 46 501 BETA-SECRETASE.
 CC DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
 CC TRANSEM 458 478 POTENTIAL.
 CC DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
 CC ACT_SITE 93 93 BY SIMILARITY.
 CC ACT_SITE 289 289 BY SIMILARITY.
 CC DISULFID 216 420 BY SIMILARITY.
 CC DISULFID 278 443
 CC DISULFID 330 380
 CC CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 146 189 Missing (in isoform C and isoform D).
 FT VARSPLIC 190 214 /FtId=VSP_005222.
 FT VARSPLIC 190 214 Missing (in isoform B and isoform D).
 FT VARSPLIC 190 214 /FtId=VSP_005223.
 SQ SEQUENCE 501 AA; 55763 MW; 377CB4CB24ACEF05 CRC64;
 Query Match 54.7%; Score 35; DB 1; Length 501;
 Best local similarity 44.4%; Pred. No. 1.7e+02;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 WYDPLTKLM 9
 DB 250 WYTPRRRW 258
 RESULT 74
 BACE_MOUSE STANDARD; PRT; 501 AA.
 ID BACE_MOUSE
 AC P56818
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Beta-secretase precursor (EC 3.4.23.46) (Beta-site APP cleaving
 DE enzyme) (Beta-site amyloid precursor protein cleaving enzyme)
 DE (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic
 DE protease 2) (Memapsin-2).
 GN BACE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20002972; PubMed=10531052;
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Denis P., Teplow D.B., Robu S., Amarante P., Loeffler R., Luo Y.,
 RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J.R., Rogers G., Citron M.;
 RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 RT the transmembrane aspartic protease BACE.";
 RL Science 286:735-741(1999).
 RN [2]
 RP REVISIONS TO 6 AND 81-87.
 RA Bennett B.D., Vassar R., Citron M.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057170; PubMed=10591213;
 RA Yan R., Bienkowski M.U., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
 RA Brishler J.R., Strattan N.C., Mathews W.R., Buhl A.B., Carter D.B.,
 RA Tomasekelli A.G., Parodi L.A., Heintz R.L., Gurney M.E.;
 RT "Membrane-anchored aspartyl protease with Alzheimer's disease
 RT beta-secretase activity.";
 RL Nature 402:533-537(1999).
 CC -1- FUNCTION: Responsible for the proteolytic processing of the
 CC amyloid precursor protein (APP). Cleaves at the amino terminus of
 CC the A-beta peptide sequence, between residues 671 and 672 of APP,
 CC leads to the generation and extracellular release of beta-cleaved
 CC soluble APP, and a corresponding cell-associated carboxy-terminal
 CC fragment which is later release by gamma-secretase (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
 CC Val-Aen-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
 CC Alzheimer's amyloid precursor protein.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Brain.
 CC -1- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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DR EMBL; AF190726; AAF04144.1; -
 DR EMBL; AF200346; AAF1082.1; -
 DR HSSP; P56272; IAMS.
 DR MEROPS; A01.004; -
 DR MGD; MG1.134542; Bace.
 DR InterPro; IPR001369; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 DR Hydrolyase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 KW Signal.
 KM SIGNAL.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 45 POTENTIAL.
 FT CHAIN 46 501 BETA-SECRETASE.
 FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 458 478 POTENTIAL.
 FT DOMAIN 479 501 POTENTIAL.
 FT ACT_SITE 93 93 CYTOPLASMIC (POTENTIAL).
 FT ACT_SITE 289 93 BY SIMILARITY.
 FT ACT_SITE 289 93 BY SIMILARITY.
 FT DISULFID 216 420 BY SIMILARITY.
 FT DISULFID 278 443 BY SIMILARITY.
 FT CARBOHYD 330 380 BY SIMILARITY.
 FT CARBOHYD 172 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 501 AA; 55747 MW; C085A013145E474E CRC64;

Query Match 54.7%; Score 35; DB 1; Length 501;
 Best Local Similarity 44.4%; Pred. No. 1.7e+02;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9
 DB 250 WYTPIRREW 258

RESULT 75
 BACE RAT
 AC P56819; STANDARD; PRT; 501 AA.
 ID BACE RAT
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Beta-secretase precursor (BC 3.4.23.46) (Beta-site APP cleaving
 DE enzyme) (Beta-site amyloid precursor protein cleaving enzyme)
 DE (Aspartyl) protease 2 (Asp 2) (ASP2) (Membrane-associated aspartic
 DE protease 2) (Memapsin-2).
 GN BACE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20002972; PubMed=10531052;
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Denis P., Teplow D.B., Ross S., Amarante P., Loeflof R., Luo Y.,
 RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J., Rogers G., Citron M.,
 RA "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 RA the transmembrane aspartic protease BACE".
 RL Science 286:735-741(1999).
 CC -1- FUNCTION: Responsible for the proteolytic processing of the
 CC amyloid precursor protein (APP). Cleaves at the amino terminus of

CC the A-beta peptide sequence, between residues 671 and 672 of APP,
 CC leads to the generation and extracellular release of beta-cleaved
 CC soluble APP, and a corresponding cell-associated carboxy-terminal
 CC fragment which is later release by gamma-secretase (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
 CC Val-Asn-Leu-I-Asp-Ala-Glu-Phe in the Swedish variant of
 CC Alzheimer's amyloid precursor protein.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to peptidase family A1.
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DR EMBL; AF190727; AAF04144.1; -
 DR HSSP; P32329; IYPS.
 DR MEROPS; A01.004; -
 DR InterPro; IPR001959; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 DR Hydrolyase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 KW Signal.
 KM SIGNAL.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 45 POTENTIAL.
 FT CHAIN 46 501 BETA-SECRETASE.
 FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 458 478 POTENTIAL.
 FT DOMAIN 479 501 POTENTIAL.
 FT ACT_SITE 93 93 CYTOPLASMIC (POTENTIAL).
 FT ACT_SITE 289 93 BY SIMILARITY.
 FT ACT_SITE 289 93 BY SIMILARITY.
 FT DISULFID 216 420 BY SIMILARITY.
 FT DISULFID 278 443 BY SIMILARITY.
 FT CARBOHYD 330 380 BY SIMILARITY.
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 501 AA; 55806 MW; 24B445BC8B87DB3 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 501;
 Best Local Similarity 44.4%; Pred. No. 1.7e+02;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9
 DB 250 WYTPIRREW 258

RESULT 76
 YAB4_MYCPN
 ID YAB4_MYCPN STANDARD; PRT; 524 AA.
 AC P75609;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical lipoprotein MPN084 precursor (R02_Orf524).
 GN MPN084 OR MP071.
 GN Mycoplasma pneumoniae.
 OS Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=8948633;
 RA Himmelfeich R., Hilbert H., Plegens H., Pirkl E., Li B.-C.,

RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RL pneumoniae";
CC Nucleic Acids Res. 24:4420-4449 (1996).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -1- SIMILARITY: BELONGS TO THE MG067 / MG068 / MG395 FAMILY.
CC -----
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CC -----
CC EMBL; AE000009; AAB95719.1; -.
CC PIR; S73397; S73397.
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR002414; DUF30/31.
CC Pfam; PF01727; DUF30.1.
CC Pfam; PF01732; DUF31.1.
CC PRINTS; PR00840; Y06768FAMILY.
CC DR Hypothetical protein; Lipoprotein; Membrane; Signal;
CC KW Complete proteome; Palmitate.
CC FT SIGNAL 1 21 POTENTIAL.
CC FT CHAIN 1 524 HYPOTHETICAL LIPOPROTEIN MPN084.
FT LIPID 22 22 N-palmitoyl cysteine (Potential).
FT LIPID 22 22 S-diacylglycerol cysteine (Potential).
SQ SEQUENCE 524 AA; 59553 MW; F4E7138D8092E74F CRC64;

Query Match 54.7%; Score 35; DB 1; Length 524;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 YDPLTKLM 9
DB 174 YDSLTKQW 181

RESULT 77
Y469 HUMAN STANDARD; PRT; 539 AA.
ID Y469 HUMAN STANDARD; PRT; 539 AA.
AC Q9U9FA; O75057; (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein KIAA0469.
GN KIAA0469.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=9811662; PubMed=9455484;
RA Seki N., Ohita M., Nagase T., Ishikawa K.-I., Miyajima N.,
RA Nakajima D., Nomura N., Ohara O.;
RT "Characterization of cDNA clones in size-fractionated cDNA libraries
RT from human brain.";
RL DNA Res. 4:345-349 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Wray P.;
CC Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BTB/POZ domain.
CC -1- SIMILARITY: Contains 5 Kelch repeats.
CC -----
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CC -----
CC EMBL; AB007938; BAB2314.1; -.
CC EMBL; AL031447; CAB42892.1; -.
CC InterPro; IPR000210; BTB POZ.
CC InterPro; IPR00652; Kelch_rep.
CC Pfam; PF00651; BTB; 1.
CC Pfam; PF01344; Kelch; 5.
CC SMART; SM00225; BTB; 1.
CC SMART; SM00612; Kelch; 3.
CC PROSITE; PS50097; BTB; 1.
CC DR Hypothetical protein; Kelch repeat; Repeat.
CC FT DOMAIN 35 103 BTB.
FT REPEAT 287 335
FT REPEAT 336 382
FT REPEAT 384 422
FT REPEAT 423 470
FT REPEAT 472 512
FT CONFLICT 534 534 D -> G (IN REF. 2).
SQ SEQUENCE 539 AA; 60435 MW; DDE88D184C077945 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 539;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 YDPLTKLM 9
DB 441 YDPDTLW 448

RESULT 78
YEDQ_ECO57 STANDARD; PRT; 564 AA.
ID YEDQ_ECO57 STANDARD; PRT; 564 AA.
AC O8XB92;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yedQ.
GN YEDQ OR Z3047 OR EC52694.
OS Escherichia coli O157:H7.
OC Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackatt J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lam A., Dimalanta B.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Iln J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kunara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22 (2001).
RN [3]
RP SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE YABC / YFIN (E.COIL), YHCK (B.SUBTILIS)
CC FAMILY.
CC -1- SIMILARITY: Contains 1 GGDEF domain.
CC -----

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DR EMBL; AE005417; AAG56970.1; -
DR EMBL; AP002559; BAB36117.1; -
DR PIR; P90965; P90965.
DR InterPro; IPR00160; GGDDEF.
DR Pfam; PF00990; GGDDEF.1.
DR SMART; SM00267; DUFL.1.
DR TIGRFAMs; TIGR00254; GGDDEF.1.
DR PROSITE; PS50887; GGDDEF.1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSNEM 360 380 POTENTIAL.
FT DOMAIN 428 563 GGDDEF.
SQ SEQUENCE 564 AA; 64287 MW; BBBC2286ADBAECB0 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 564;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
DB 399 WHDITLRLY 407

RESULT 79
YEDO_ECOLI
ID_YEDO_ECOLI STANDARD; PRT; 564 AA.
AC P76330; P94746;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yedQ.
GN YEDO OR B1956.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
ON NCBI_TaxID=562;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.U.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
RN [2].
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizubuchi K., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Samped G., Seki Y.,
RA Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392 (1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE YABC / YFIN (E.CODI), YHCK (B.SUBTILIS)
CC FAMILY.
CC -1- SIMILARITY: Contains 1 GGDDEF domain.
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DR EMBL; AE000287; AAC75022.1; ALT_INT.
DR EMBL; D90835; BAA15784.1; -
DR Ecogen; EG14040; yedQ.
DR InterPro; IPR00160; GGDDEF.
DR Pfam; PF00990; GGDDEF.1.
DR SMART; SM00267; DUFL.1.
DR TIGRFAMs; TIGR00254; GGDDEF.1.
DR PROSITE; PS50887; GGDDEF.1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSNEM 360 380 POTENTIAL.
FT DOMAIN 428 563 GGDDEF.
SQ SEQUENCE 564 AA; 64283 MW; 05FB02C1BE2A8938 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 564;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
DB 399 WHDITLRLY 407

RESULT 80
MIS_BOVIN
ID_MIS_BOVIN STANDARD; PRT; 575 AA.
AC P03972;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Muellerian inhibiting factor precursor (MIS) (Anti-muellerian hormone)
DE (AMH) (muellerian inhibiting substance).
GN AMH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
RX MEDLINE=86218082; PubMed=3754790;
RA Cate R.L., Mataliano R.J., Hession C., Tizard R., Farber N.M.,
RA Cheung A., Ninfa E.G., Frey A.Z., Gash D.J., Chow E.P., Fisher R.A.,
RA Beronius J.M., Torres G., Wallner B.P., Ramachandran K.L.,
RA Ragin R.C., Manganaro T.F., McLaughlin D.L., Donahoe P.K.;
RT "Isolation of the bovine and human genes for Mullerian inhibiting
RT substance and expression of the human gene in animal cells.";
RL Cell 45:685-698 (1986).
CC -1- FUNCTION: THIS GLYCOPROTEIN, PRODUCED BY THE SEROTOL CELLS OF THE
CC TESTIS, CAUSES REGRESSION OF THE MUELLERIAN DUCT. IT ALSO IS ABLE
CC TO INHIBIT THE GROWTH OF TUMORS DERIVED FROM TISSUES OF MUELLERIAN
CC DUCT ORIGIN.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- MISCELLANEOUS: Although it does not compete with EGF for receptor
CC binding sites, MIS can inhibit the autophosphorylation of the EGF
CC receptor in vitro.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
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CC BROAD-SPECTRUM PEROXIDASE ACTIVITIES. MAY PLAY A ROLE IN THE
CC INTERCELLULAR SURVIVAL OF MYCOBACTERIA (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
CC -1- COFACTOR: Binds 1 heme B (h2o-protophyrin IX) group per
CC dimer.
CC -1- SUBUNIT: Homodimer (probable).
CC -1- SIMILARITY: Belongs to the peroxidase family. Bacterial
CC peroxidase/catalase subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y07665; CA669192.1; -.
DR HSSP: P00431; 1CCK.
DR InterPro: IPR000763; Rac ctase/prase.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; Peroxidase.
DR PRINTS: PRO0458; PEROXIDASE.
DR TIGRfam: TIGR00198; cat per HPI. 1.
DR PROSITE: PS00435; PEROXIDASE_1; 1.
DR PROSITE: PS00436; PEROXIDASE_2; 1.
DR PROSITE: PS50873; PEROXIDASE_4; 1.
DR Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
FT ACT SITE 113 113
FT ACT SITE 117 117 BY SIMILARITY.
FT METAL 285 285 IRON (HEM AXIAL LGAND).
SQ SEQUENCE 752 AA; 83100 MW; B66BAD3DD26E70D CRC64;

Query Match 54.7%; Score 35; DB 1; Length 752;
Best Local Similarity 55.6%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 2 YDPLTKLML 10
Db 403 YGPITRML 411

RESULT 83
KHL5 HUMAN STANDARD: PRT; 755 AA.
AC Q96PQ7; O86XW0; Q9NWK3; Q9NWK7; Q9NWA9; Q9YX2;
CT 28-FEB-2003 (Rel. 41, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Kelch-like protein 5.
GN KHL5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Fetal brain;
RX MEDLINE=21474935; PubMed=11590829;
RA Wang S., Zhou Z., Ying K., Tang R., Huang Y., Wu C., Xie Y., Mao Y.;
RT "Cloning and characterization of KHL5, a novel human gene encoding a
RT kelch-related protein with a BTB domain.";
RL Biochem. Genet. 39:227-238(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 212-755 FROM N.A. (ISOFORM 1), AND SEQUENCE OF 476-755
RP FROM N.A. (ISOFORM 2).
RC TISSUE=Placenta;
RA Isegawa T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H.,

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RA Magatsuna M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto K., Wakamatsu A., Nakamura Y., Nagahari K., Maeno Y.,
RA Nimomura K., Iwayanagi T.;
RT "NEO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 383-755 FROM N.A. (ISOFORM 1).
RC TISSUE=uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cassavant T.L., Scheetz T.E.,
RA Brownstein W.J., Uedlin T.B., Toshlyuk S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollay S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Fahy J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield A.S.N., Krzywnicki M.I., Skalski U., Smalins D.E.,
RA "Generation and initial analysis of more than 15,000 full-length human
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 490-755 FROM N.A. (ISOFORM 3).
RC TISSUE=tongue;
RA Jiyi Y., Lianxian C., Zhengjian Z., Bo Y.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q96PQ7-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q96PQ7-2; Sequence=VSP_008619;
CC Note=May be due to intron retention. No experimental
CC confirmation available;
CC Name=3;
CC IsoId=Q96PQ7-3; Sequence=VSP_008620;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Expressed in adrenal gland, ovary and thyroid
CC gland and less abundantly in lymph node, prostate, spinal chord,
CC testis and trachea.
CC -1- SIMILARITY: Contains 1 BTB/POZ domain.
CC -1- SIMILARITY: Contains 6 Kelch repeats.
CC -1- CAUTION: Ref.1 (AAU08584) sequence differs from that shown due to
CC a stop codon in position 735 which was translated as Trp to extend
CC the sequence.
CC -----
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CC -----
DR EMBL: AF272976; AL008584.1; ALT TERM.
DR EMBL: AC079921; -. NOT ANNOTATED CDS.
DR EMBL: AK001698; BAA91845.1; ALT INIT.
DR EMBL: AK001836; BAA91933.1; ALT INIT.
DR EMBL: AK002174; BAA92121.1; ALT INIT.
DR EMBL: BC048262; AAH48262.1; -.
DR EMBL: AF123320; AAD32565.1; ALT INIT.
DR EMBL: HGNC:6356; KHL5.
DR Genew; HGNC:6356; KHL5.
MIM; 608064; -.

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DR GO; GO:0005737; C:cytoplasm; ISS.
DR GO; GO:0003779; P:actin binding; ISS.
DR GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; ISS.
DR InterPro; IPR000210; BTB_Poz.
DR InterPro; IPR006651; Kelch.
DR InterPro; IPR006652; Kelch_rep.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF01344; Kelch; 6.
DR PRINTS; PR00501; KETCHREPEAT.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00612; Kelch; 6.
DR PROSITE; PS50097; BTB; 1.
KW Cytoskeleton; Actin-binding; Repeat; Kelch repeat;
Alternative splicing;
FT DOMAIN 220 287 BTB.
FT REPEAT 468 514 KELCH 1.
FT REPEAT 515 561 KELCH 2.
FT REPEAT 563 608 KELCH 3.
FT REPEAT 609 655 KELCH 4.
FT REPEAT 657 708 KELCH 5.
FT REPEAT 709 754 KELCH 6.
FT VARSPLIC 739 755 APLCGRAGACVTVTKL -> WHSCFIITLTLFLKKOPLM
(in isoform 2).
FT VARSPLIC 739 755 /FTID=VSP_008619.
FT VARSPLIC 739 755 APLCGRAGACVTVTKL -> FSHTFEDSKHLVAIKQTIV
RONSLSSEFRSH (in isoform 3).
FT VARSPLIC 739 755 /FTID=VSP_008620.
FT CONFLICT 10 10 I -> L (IN REF. 1).
FT CONFLICT 323 323 L -> P (IN REF. 3; BAA91845).
FT CONFLICT 435 435 Q -> R (IN REF. 1).
FT CONFLICT 594 594 M -> K (IN REF. 3; BAA91845).
FT CONFLICT 695 695 S -> G (IN REF. 3; BAA92121).
SQ SEQUENCE 755 AA; 84457 MW; 2A81BFB98F387F6C CRC64;

Query Match 54.7%; Score 35; DB 1; Length 755;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLM 9
Db 681 YDPKTDWM 688

RESULT 84
41_XENLA STANDARD; PRT; 801 AA.
ID 41_XENLA
AC P11434;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytoskeletal protein 4.1 (Band 4.1).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCB1_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90249600; Pubmed=2186944;
RA Spencer M., Giebelhaus D.H., Kelly G.M., Bicknell J., Florio S.K.,
RA Bunt-Milam A., Moon R.T.;
RA "Membrane skeleton protein 4.1 in developing Xenopus: expression in
RT postmitotic cells of the retina.";
RL Dev. Biol. 139:279-291(1990).
[2]
RN [2]
RP SEQUENCE OF 1-550 FROM N.A.
RX MEDLINE=88223353; Pubmed=2453290;
RA Giebelhaus D.H., Eib D.W., Moon R.T.;
RA "Antisense RNA inhibits expression of membrane skeleton protein 4.1
RT during embryonic development of Xenopus.";
RL Cell 53:601-615(1988).
CC -1- FUNCTION: Protein 4.1 is a major structural element of the
erythrocyte membrane skeleton. It plays a key role in regulating
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CC membrane physical properties of mechanical stability and
CC deformability by stabilizing spectrin-actin interaction. Binds
CC with a high affinity to glycophorin and with lower affinity to
CC band III protein.
CC -1- TISSUE SPECIFICITY: Found exclusively in photoreceptors following
CC the terminal mitosis of retinal neurons. When retinal
CC synaptogenesis is complete, protein 4.1 is also expressed in the
CC inner retina. In adult amphibian retinas, protein 4.1 is detected
CC in photoreceptors, bipolar cells, and ganglion cell axons.
CC -1- PTM: Phosphorylated at multiple sites by different protein kinases
CC and each phosphorylation event selectively modulates the protein's
CC functions.
CC -1- SIMILARITY: Contains 1 FERM domain.
CC -----
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CC -----
CC EMBL; M20621; AAA49695.1; -.
CC PIR; A37353; A37353.
CC InterPro; IPR008379; 4_1_CTD.
CC InterPro; IPR000299; Band_4.1.
CC InterPro; IPR007477; SAB.
CC Pfam; PF05902; 4_1_CTD; 1.
CC Pfam; PF00373; Band_4.1; 1.
CC Pfam; PF04382; SAB; 1.
CC PRINTS; PR00935; BAND4.1.
CC SMART; SM00295; B41; 1.
CC PROSITE; PS00660; FERM_1; 1.
CC PROSITE; PS00661; FERM_2; 1.
CC PROSITE; PS50057; FERM_3; 1.
KW Structural protein; Cytoskeleton; Actin-binding; Phosphorylation.
FT DOMAIN 193 474 FERM.
FT DOMAIN 477 587 HYDROPHILIC.
FT DOMAIN 588 651 SPECTRIN-ACTIN-BINDING.
FT DOMAIN 653 801 CARBOXYL-TERMINAL (CTD).
SQ SEQUENCE 801 AA; 89429 MW; 07FA508552359A0F CRC64;

Query Match 54.7%; Score 35; DB 1; Length 801;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 10
Db 239 WESPCKVWL 248

RESULT 85
DMSA_RHOSH STANDARD; PRT; 822 AA.
ID DMSA_RHOSH
AC O5736;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Dimethyl sulfoxide reductase precursor (EC 1.8.99.-) (DMSO reductase)
DE (DMSOR).
CN DMSA OR DMSA.
OS Rhodospirillum rubrum (Rhodospirillum rubrum).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirales;
OC Rhodospiraceae; Rhodospirillum.
OC NCB1_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=f. sp. denitrificans IL106;
RX MEDLINE=96248388; Pubmed=8645727;
RA Hilton J.C., Rajagopalan K.V.;
RA "Molecular cloning of dimethyl sulfoxide reductase from Rhodospirillum
RT rubrum. Biochem. Acta 1294:111-114(1996).
RL Biochim. Biophys. Acta 1294:111-114(1996).
```

[2] SEQUENCE FROM N.A., SEQUENCE OF N-TERMINUS, AND PARTIAL SEQUENCE.
RP STRAIN-IL106;
RX MEDLINE=96068928; PubMed=8534974;
RA Yamamoto I., Wada N., Ujiye T., Tachibana M., Matsuzaki M.,
RT Kajiwara H., Watanabe Y., Hirano H., Okubo A., Satoh T., Yamazaki S.,
RT "Cloning and nucleotide sequence of the gene encoding dimethyl
RT sulfoxide reductase from Rhodospirillum rubrum F. sp.
RT dehydrificans";
RU Biochem. Biotechnol. Biochem. 59:1850-1855(1995).
[3]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=96247313; PubMed=8658134;
RA Schindelin H., Kisker C., Hilton J., Rajagopalan K.V., Rees D.C.,
RT "Crystal structure of DMSO reductase: redox-linked changes in
RT molybdopterin coordination.";
RU Science 272:1615-1621(1996).
[4]
RP X-RAY CRYSTALLOGRAPHY (1.3 ANGSTROMS).
RA Li H.-K., Temple C., Rajagopalan K.V., Schindelin H.,
RT "The 1.3 A crystal structure of Rhodospirillum rubrum dimethyl
RT sulfoxide reductase reveals two distinct molybdenum coordination
RT environments.";
RU J. Am. Chem. Soc. 122:7673-7680(2000).
CC -1- FUNCTION: Terminal reductase during anaerobic growth on
CC various sulfoxide and N-oxide compounds.
CC -1- CATALYTIC ACTIVITY: Reduces various N-oxide and sulfoxide
CC compounds including trimethylamine N-oxide.
CC -1- COFACTOR: Molybdenum (molybdopterin).
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Periplasmic.
CC -1- PTM: Predicted to be exported by the Tat system. The position of
CC the signal peptide cleavage has been experimentally proven.
CC -1- SIMILARITY: Belongs to the prokaryotic molybdopterin-containing
CC oxidoreductase family.

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EMBL: LA6851; AAB07230.1; -
EMBL: D38634; BAA07615.1; -
PDB: 1E01; 03-OCT-01.
DR InterPro: IPR009010; Asp decarb_fold.
DR InterPro: IPR006658; Biac.
DR InterPro: IPR006657; Mol dinuc_bind.
DR InterPro: IPR006656; Molybdopterin.
DR InterPro: IPR006655; Prok_Mboxred.
DR InterPro: IPR006311; Tat.
DR Pfam: PF00384; molybdopterin; 1.
DR Pfam: PF01568; Molybdop binding; 1.
DR TIGRFAMs: TIGR00509; biac fam; 1.
DR TIGRFAMs: TIGR01409; Tat signal seq; 1.
DR PROSITE: PS00551; MOLYBDOPTERIN_PROK_1; FALSE_NEG.
DR PROSITE: PS00490; MOLYBDOPTERIN_PROK_2; 1.
DR PROSITE: PS00932; MOLYBDOPTERIN_PROK_3; 1.
KM Oxidoreductase; Molybdenum; Periplasmic; Signal; 3D-structure.
FT SIGNAL 1 42
FT CHAIN 43 822 DIMETHYL SULFOXIDE REDUCTASE.
FT ACT SITE 189 189
FT STRAND 48 54
FT TURN 55 56
FT STRAND 57 64
FT TURN 65 66
FT STRAND 67 73
FT TURN 75 76
FT TURN 82 83
FT HELIX 84 89

FT TURN 90 92
FT TURN 94 95
FT STRAND 96 96
FT STRAND 101 103
FT HELIX 104 109
FT HELIX 110 112
FT HELIX 115 117
FT TURN 118 119
FT STRAND 123 125
FT HELIX 128 129
FT HELIX 148 150
FT STRAND 151 152
FT HELIX 167 178
FT TURN 179 179
FT STRAND 182 185
FT TURN 191 192
FT HELIX 193 200
FT TURN 201 201
FT TURN 206 207
FT HELIX 213 219
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FT STRAND 501 501
FT STRAND 503 503
FT TURN 506 509
FT TURN 510 510
FT STRAND 513 517
FT STRAND 520 522
FT HELIX 525 529
FT STRAND 531 533
FT TURN 536 540
FT TURN 548 549
FT STRAND 551 551
FT HELIX 553 563

FT TURN 564 565
FT HELIX 567 571
FT TURN 572 573
FT HELIX 576 575
FT TURN 594 595
FT HELIX 601 607
FT STRAND 609 611
FT HELIX 616 619
FT TURN 622 623
FT HELIX 624 628
FT TURN 630 632
FT TURN 638 639
FT STRAND 642 643
FT HELIX 647 652
FT TURN 655 656
FT TURN 670 671
FT TURN 673 674
FT STRAND 679 682
FT STRAND 690 690
FT TURN 691 692
FT STRAND 693 693
FT TURN 694 696
FT HELIX 698 702
FT TURN 703 703
FT STRAND 705 705
FT TURN 706 707
FT STRAND 708 708
FT STRAND 710 713
FT HELIX 715 719
FT TURN 720 722
FT TURN 725 726
FT STRAND 728 732
FT STRAND 737 744
FT TURN 746 747

Query Match 54.7%; Score 35; DB 1; Length 822;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPL 5
Db 760 WYDPL 764

RESULT 86
EF2_BETVU STANDARD; PRT; 843 AA.
ID EF2_BETVU
AC 023755;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor 2 (EF-2).
OS Beta vulgaris (Sugar beet).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Beta.
OX NCBI_TaxID=161934;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root;
RA Vogel R.; Rausch T.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: Phosphorylation by EF-2 kinase completely inactivates EF-2
CC (by similarity).
CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
CC -----
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CC -----
DR EMBL; Z97178; CAB09900.1; -;
DR PIR; T14579; T14579.
DR InterPro; IPR000795; EF_GTPbind.
DR InterPro; IPR000640; EFG_C.
DR InterPro; IPR009022; EFG_III_V.
DR InterPro; IPR005517; EFG_IV_1.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR009000; Translat_factor.
DR Pfam; PF00679; EFG_C_1.
DR Pfam; PF03764; EFG_IV_1.
DR Pfam; PF00009; GTP_BETVU_1.
DR Pfam; PF03144; GTP_BETVU_D2_1.
DR PRINTS; PR00315; ELONGATNFCT.
DR PROSITE; PS00301; EFACITOR_GTP_1.
KM Elongation factor; GTP-binding; Protein biosynthesis; Phosphorylation.
FT NP_BIND 26 33 GTP. (BY SIMILARITY).
FT NP_BIND 104 108 GTP (BY SIMILARITY).
FT NP_BIND 158 161 GTP (BY SIMILARITY).
FT MOD_RES 57 57 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 59 59 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 700 700 DIPHTHAMIDE (BY SIMILARITY).
SQ SEQUENCE 843 AA; 93799 MW; D11325B42A51F4F8 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 843;
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9
Db 249 FPDPAKKM 257

RESULT 87
POL_MPMV STANDARD; PRT; 867 AA.
ID POL_MPMV
AC P07572;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE POL polypeptide (Contains: Reverse transcriptase (EC 2.7.7.49);
DE Endonuclease).
GN POL.
OS Simian Mason-Pfizer virus (MPMV).
OC Viruses; Retroid viruses; Retroviridae; Betaretrovirus.
OX NCBI_TaxID=11855;
RN [1]
RP SEQUENCE FROM N.A. (CLONE 6A).
RX MEDLINE=86189951; PubMed=2421920;
RA Sonigo P.; Barker C.; Hunter E.; Main-Hobson S.;
RT "Nucleotide sequence of Mason-Pfizer monkey virus: an
RT immunosuppressive D-type retrovirus.";
RL Cell 45:375-385(1986).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA} (N).
CC -1- PMT: Specific enzymatic cleavages in vivo yield mature proteins.
CC -----
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CC -----
DR EMBL; M12349; AAA47711.1; -;
DR PIR; C25839; GNLJMP.
DR HSPD; P03355; IMWL.

DR InterPro: IPR001037; Integrase_C.
 DR InterPro: IPR003308; Integrase_Zn.
 DR InterPro: IPR002156; RNaseH.
 DR InterPro: IPR001584; Rve.
 DR InterPro: IPR000477; RYase.
 DR Pfam: PF00552; Integrase_1.
 DR Pfam: PF02022; Integrase; 1.
 DR Pfam: PF00075; Integrase; 1.
 DR Pfam: PF00665; rve; 1.
 DR Pfam: PF00078; rve; 1.
 DR Transferrase; RNA-directed DNA polymerase; Hydrolase; Nuclease;
 KW Endonuclease; Polypeptide.
 SQ SEQUENCE 867 AA; 98404 MW; 0F5EDFC7B97935 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 867;
 Best Local Similarity 55.6%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 WYDPLTKLM 9
 DB 816 WKDPLDNTW 824

RESULT 88
 ID POL_SRV1 STANDARD; PRT; 867 AA.
 AC P04025;
 DT 23-OCT-1996 (Rel. 02, Created)
 DT 23-OCT-1996 (Rel. 02, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE POL polyprotein [Contains: Reverse transcriptase (EC 2.7.7.49);
 DE Endonuclease].
 GN POL.
 OS Simian retrovirus SRV-1.
 OC Viruses; Retrovirdae; Betaretrovirus.
 CC NCBI_Taxid=11942;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86151668; PubMed=3006247;
 RA Power M.D., Marx P.A., Bryant M.L., Gardner M.B., Barr P.J.,
 RA Luciw P.A.;
 RT Nucleotide sequence of SRV-1, a type D simian acquired immune
 RT deficiency syndrome retrovirus.;
 RL Science 231:1567-1572(1986).
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + [DNA] (N).
 CC -1- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
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 CC EMBL: M1841; AAA47732.1; -
 DR HSSP: P03355; 1MMI.
 DR InterPro: IPR001037; Integrase_C.
 DR InterPro: IPR003308; Integrase_Zn.
 DR InterPro: IPR002156; RNaseH.
 DR InterPro: IPR001584; Rve.
 DR InterPro: IPR000477; RYase.
 DR Pfam: PF00552; Integrase_1.
 DR Pfam: PF02022; Integrase; 1.
 DR Pfam: PF00075; Integrase; 1.
 DR Pfam: PF00665; rve; 1.
 DR Pfam: PF00078; rve; 1.
 DR Transferrase; RNA-directed DNA polymerase; Hydrolase; Nuclease;
 KW Endonuclease; Polypeptide.
 SQ SEQUENCE 867 AA; 98361 MW; ABB06A0B770A6473 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 867;

Best Local Similarity 55.6%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 WYDPLTKLM 9
 DB 816 WKDPLDNTW 824

RESULT 89
 ID POL_SRV2 STANDARD; PRT; 867 AA.
 AC P51517;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE POL polyprotein [Contains: Reverse transcriptase (EC 2.7.7.49);
 DE Endonuclease].
 GN POL.
 OS Simian retrovirus SRV-2.
 OC Viruses; Retrovirdae; Betaretrovirus.
 CC NCBI_Taxid=39068;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87151131; PubMed=2435057;
 RA Thayer R.M., Power M.D., Bryant M.L., Gardner M.B., Barr P.J.,
 RA Luciw P.A.;
 RT "Sequence relationships of type D retroviruses which cause simian
 RT acquired immunodeficiency syndrome.";
 RL Virology 157:317-329(1987).
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + [DNA] (N).
 CC -1- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
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 CC EMBL: M16605; AAA47562.1; -
 DR HSSP: P03355; 1MMI.
 DR InterPro: IPR001037; Integrase_C.
 DR InterPro: IPR003308; Integrase_Zn.
 DR InterPro: IPR002156; RNaseH.
 DR InterPro: IPR001584; Rve.
 DR InterPro: IPR000477; RYase.
 DR Pfam: PF00552; Integrase_1.
 DR Pfam: PF02022; Integrase; 1.
 DR Pfam: PF00075; Integrase; 1.
 DR Pfam: PF00665; rve; 1.
 DR Pfam: PF00078; rve; 1.
 DR Transferrase; RNA-directed DNA polymerase; Hydrolase; Nuclease;
 KW Endonuclease; Polypeptide.
 SQ SEQUENCE 867 AA; 98038 MW; F64227F7365F3659 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 867;
 Best Local Similarity 55.6%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 WYDPLTKLM 9
 DB 816 WKDPLDNTW 824

RESULT 90
 ID JAK1_MOUSE STANDARD; PRT; 1153 AA.
 AC P53332; O62126;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Tyrosine-protein kinase JAK1 (EC 2.7.1.112) (Janus kinase 1) (JAK-1).
 GN JAK1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93322747; PubMed=8331382;
 RA Yang X., Chung D., Cepko C.L.;
 RT "Molecular cloning of the murine JAK1 protein tyrosine kinase and its
 expression in the mouse central nervous system."; J. Neurosci. 13:3006-3017(1993).
 RL [2]
 RP SEQUENCE OF 999-1069 FROM N.A.
 RX MEDLINE=90152381; PubMed=2482828;
 RA Wilks A.F., Kurban R.R., Hovens C.M., Ralph S.J.;
 RT "The application of the polymerase chain reaction to cloning members
 of the protein tyrosine kinase family."; Gene 85:67-74(1989).
 RL [3]
 RP SEQUENCE OF 999-1069 FROM N.A.
 RX MEDLINE=89160824; PubMed=2466296;
 RA Wilks A.F.;
 RT "Two putative protein-tyrosine kinases identified by application of
 the polymerase chain reaction."; Proc. Natl. Acad. Sci. U.S.A. 86:1603-1607(1989).
 RL [1]
 CC -1 FUNCTION: Tyrosine kinase of the non-receptor type, involved in
 the TNF-alpha/beta/gamma signal pathway. Kinase partner for the
 interleukin (IL)-2 receptor.
 CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 tyrosine phosphate.
 CC -1 SUBCELLULAR LOCATION: Wholly intracellular, possibly membrane
 associated.
 CC -1 DOMAIN: Possesses two phosphotransferase domains. The second one
 probably contains the catalytic domain (By similarity), while the
 presence of slight differences suggest a different role for domain
 1.
 CC -1 SIMILARITY: Belongs to the Tyr family of protein kinases. JAK
 subfamily.
 CC -1 SIMILARITY: Contains 1 SH2 domain.
 CC -1 SIMILARITY: Contains 1 FERM domain.
 CC -----
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 CC -----
 CC EMBL: S63728; AAB27517.2; -;
 DR EMBL: M33425; AAA40016.1; -;
 DR HSSP: P11362; IFCK.
 DR MGD: MGI:96628; Jak1.
 DR InterPro: IPR000299; Band 4.1.
 DR InterPro: IPR00719; Prot_Kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR008266; Tyr_kinase_AS.
 DR Pfam: PF00069; Pkinase; 2.
 DR Pfam: PF00017; SH2; 1.
 DR PRINTS: PRO00109; TYRKINASE.
 DR PRODOM: PD000001; Prot_Kinase; 2.
 DR PRODOM: PD000093; SH2; 1.
 DR SMART: SM00295; B41; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00660; FERM_1; FALSE NEG.
 DR PROSITE: PS00661; FERM_2; FALSE NEG.
 DR PROSITE: PS00507; FERM_3; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 2.

DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00001; SH2; 1.
 KM Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 GN SH2 domain; Repeat.
 FT DOMAIN 34 420 FERM.
 FT DOMAIN 334 362 HIGHLY CHARGED.
 FT DOMAIN 439 528 SH2 (ATYPICAL).
 FT DOMAIN 582 854 PROTEIN KINASE 1.
 FT DOMAIN 874 1152 PROTEIN KINASE 2.
 FT NP_BIND 880 888 ATP (BY SIMILARITY).
 FT BINDING 907 907 ATP (BY SIMILARITY).
 FT ACT_SITE 1002 1002 BY SIMILARITY.
 FT MOD_RES 1033 1033 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CONFLICT 999 999 V->I (IN REF. 2 AND 3).
 FT CONFLICT 1068 1069 VT->IP (IN REF. 2 AND 3).
 SQ SEQUENCE 1153 AA; 133367 MW; 0B9816A5B3868B CRC64;
 Query Match 54.7%; Score 35; DB 1; Length 1153;
 Best Local Similarity 75.0%; Pred. No. 4e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 YDPLTKLM 9
 DB 81 YDESTKLM 88
 RESULT 91
 ID KXELC DROME STANDARD; PRT; 1477 AA.
 AC 004652; 004653; 086PA7; 09VJA2;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ring canal kelch protein [Contains: Kelch short protein].
 GN KXEL OR CG7210.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=93201592; PubMed=8453663;
 RA Xue F., Cooley L.;
 RT "Kelch encodes a component of intercellular bridges in Drosophila egg
 RT chambers."; Cell 72:681-693(1993).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adamatides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman W.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale I., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Caden E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howard T.J., Wei M.-H., Ibegwam C.,
 RA Jaiswal M., Kalish F., Karen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklow G., Mishina N.V., Mohanty C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye U., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RT Science 287:2185-2195 (2000).
RN [3]
RP REVISIONS.
RX MEDLINE=22426069; PubMed=12537572;
RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.B.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bertencourt B.R., Celinker S.B., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter U., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley; TISSUE=Embryo;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R.A., Gonzalez M., Guarin H., Krommiller B. L. P.W., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacleb J.M., Pargass V., Park S.,
RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
RA Celinker S.E.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP CHARACTERIZATION.
RC TISSUE=Embryo;
RX MEDLINE=97236487; PubMed=9118811;
RA Robinson D.N., Cooley L.;
RT "Examination of the function of two kelch proteins generated by stop
RT codon suppression.";
RL Development 124:1405-1417 (1997).
CC -!- FUNCTION: Component of ring canals that regulates the flow of
CC cytoplasm between cells. May be involved in the regulation of
CC cytoplasm flow from nurse cells to the oocyte during oogenesis.
CC Binds actin.
CC -!- SUBCELLULAR LOCATION: Inner surface of cytoplasmic bridges or ring
CC canals present in egg chambers. Subcortically in imaginal disk
CC epithelia.
CC -!- TISSUE SPECIFICITY: Both proteins are expressed in ovaries, male
CC testis, ovariectomized females, cuticle, salivary gland and
CC imaginal disks. Kelch short protein is the predominant form and
CC is also expressed in fat bodies. On entry into metamorphosis
CC levels of full length protein increase in testis and imaginal
CC disks.
CC -!- DEVELOPMENTAL STAGE: Larvae, pupae and adults.
CC -!- SIMILARITY: Contains 1 BTB/POZ domain.
CC -!- SIMILARITY: Contains 6 Kelch repeats.
CC -!- CAUTION: Ref.5 believes residue 690 is a selenocysteine.
CC -----
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CC -----
DR EMBL; L08483; AAA53471.1; -
DR EMBL; L08483; AAA53472.2; -
DR EMBL; AE003657; AAF53651.1; -
DR EMBL; AE003657; AAF53651.1; -
DR EMBL; BT003250; AA025007.1; ALT_SEQ.
DR HSSP; 005516; IC53.
DR FlyBase; FBgn000301; kel.
DR GO; GO:0007292; P:female gamete generation; IMP.
DR GO; GO:0007301; P:ovarian ring canal formation; IDA.
DR InterPro; IPR000210; BTB POZ.
DR InterPro; IPR006651; Kelch.
DR InterPro; IPR006652; Kelch_rep.
DR Pfam; PF00651; BTB, 1.
DR Pfam; PF01344; Kelch, 6.
DR PRINTS; PR00501; KELCHREPEAT.
DR SMART; SM00225; BTB, 1.
DR SMART; SM00612; Kelch; 6.
DR PROSITE; PS50097; BTB, 1.
KW Cytoskeleton; Actin-binding; Selenium; Selenocysteine; Kelch repeat;
KW Repeat.
FT CHAIN 1 1477
FT 1 689
FT DOMAIN 157 223
FT REPEAT 404 449
FT REPEAT 450 496
FT REPEAT 498 543
FT REPEAT 545 592
FT REPEAT 594 639
FT REPEAT 641 687
FT DOMAIN 18 28
FT DOMAIN 29 87
FT DOMAIN 29 36
FT DOMAIN 78 83
FT SE_CYS 690 690
FT CONFLICT 493 493
FT CONFLICT 596 596
FT CONFLICT 824 824
FT CONFLICT 858 858
FT CONFLICT 1083 1083
FT CONFLICT 1086 1086
SQ SEQUENCE 1477 AA; 160086 MW; 4851EEAE999DBA47 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 1477;
Best Local Similarity 62.5%; Pred. NO. 5.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLW 9
Db 516 YDPKTDIW 523

RESULT 92
ID UBR1_KULU STANDARD; PRT; 1941 AA.
AC 060014;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE N-end-recognizing protein (UBiqtlin-protein ligase E3 component) (N-
DE recognin).
GN UBR1.
OS Kluyveromyces fragilis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28995;
RN [1]
RP SEQUENCE FROM N.A.
RA Waller P.R.H., Varshavsky A.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Recognition component of the N-end rule pathway. Binds
CC to proteins bearing amino-terminal residues that are destabilizing
CC according to the N-end rule, but does not bind to otherwise

identical proteins bearing stabilizing amino-terminal residues.
-1- SIMILARITY: Contains 1 UBR1-type zinc finger.

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DR EMBL; AF061554; AAC15841.1; -
DR PIR; T30554; T30554.
DR InterPro; IPR003126; Znf_Nrecoznln.
DR InterPro; IPR001841; Znf_Tring.
DR Pfam; PF02207; Zf-UBR1; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00396; Znf_UBR1; 1.
KW Ligase; Ubl conjugation pathway.
SQ SEQUENCE 1941 AA; 223682 MW; 37C2E1BCA0803268 CRC64;
Query Match 54.7%; Score 35; DB 1; Length 1941;
Best Local Similarity 55.6%; Pred. No. 6; 9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YDPLTKML 10
Db 1748 YEHLRLMI 1756

RESULT 93
Y960_HAEIN STANDARD; PRT; 116 AA.
ID Y960_HAEIN STANDARD; PRT; 116 AA.
AC P44084;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein H10960 precursor.
GN H10960.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleisemann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodex A., Kelley U.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,
RA Utecherback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).

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DR EMBL; U32777; AAC22628.1; -
DR PIR; C64017; C64017.
DR TIGR; H10960; -
DR InterPro; IPR000437; Prok_lipoprot_S.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; UNKNOWN_1.

Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 116 HYPOTHEETICAL PROTEIN H10960.
SQ SEQUENCE 116 AA; 13498 MW; 97214FD32CE8C25F CRC64;
Query Match 53.1%; Score 34; DB 1; Length 116;
Best Local Similarity 54.5%; Pred. No. 57;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

Qy 1 WYDPL--TKM 9
Db 68 WYDHLGVTOIW 78

RESULT 94
SP2G_BACTK STANDARD; PRT; 161 AA.
ID SP2G_BACTK STANDARD; PRT; 161 AA.
AC P26767;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Possible sporulation sigma factor processing peptidase (EC 3.4.23.-)
DE (Fragment).
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-1-Dipfel;
RX MEDLINE=91267951; PubMed=1904859;
RA Adams L.F., Brown K.L., Whiteley H.R.;
RT "Molecular cloning and characterization of two genes encoding sigma
RT factors that direct transcription from a Bacillus thuringiensis
RT crystal protein gene promoter.";
RL J. Bacteriol. 173:3846-3854(1991).
CC -1- FUNCTION: PROBABLY ACTIVATES THE RNA POLYMERASE SIGMA-35 FACTOR
CC AT THE STAGE II OF SPOULATION.
CC -1- SIMILARITY: TO B SUBTILIS SPOTIGA.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY U4. IT IS POSSIBLE THAT
CC THIS IS AN ASPARTYL PROTEASE.

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DR EMBL; X56697; CAA40025.1; -
DR PIR; D39441; D39441.
DR MEROPS; U04.001; -
DR InterPro; IPR005081; Peptidase_U4.
DR Pfam; PF03419; Peptidase_U4; 1.
KW Sporulation; Hydrolase; Aspartyl protease.
FT NON_TER 1
FT ACT_SITE 38 38 BY SIMILARITY.
SQ SEQUENCE 161 AA; 18182 MW; 09945F97F64FFBF CRC64;
Query Match 53.1%; Score 34; DB 1; Length 161;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YDPLTK 7
Db 44 YDPLTK 49

RESULT 95
RNH2_PYRAB STANDARD; PRT; 224 AA.
ID RNH2_PYRAB STANDARD; PRT; 224 AA.
AC Q9VIA9;
DT 16-OCT-2001 (Rel. 40, Created)

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DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Ribonuclease H1 (EC 3.1.26.4) (Rnase H1).
GN RNBH OR PYRAB05180 OR PAB0352.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GBS / Orsay;
RX MEDLINE=22511545; PubMed=12622808;
RA Cohen G.N., Barde V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA Van der Oost J., Weissenbach J., Zivanovic Y., Forrester P.,
RT "An integrated analysis of the genome of the hyperthermophilic
archaeon Pyrococcus abyssi."
RL Mol. Microbiol. 47:1495-1512(2003).
CC -1- FUNCTION: This enzyme is an endonuclease that degrades the RNA of
CC -1- RNA-DNA hybrids specifically (By similarity).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphomonoester
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the Rnase H1 family.
CC -----
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CC -----
DR EMBL: AJ248284; CAB49440.1; -.
DR PIR: A75170; A75170.
DR HSSP: O57599; 1EKE.
DR HAMAP: MF_00052; -.
DR InterPro: IPR001352; Rnase_H1/H11.
DR InterPro: IPR004649; Rnh1.
DR Pfam: PF01351; Rnase_H1; 1.
DR TIGRFAMs: TIGR00729; TIGR00729; 1.
DR HydroLase; Nuclease; Endonuclease; Complete proteome.
FT ACT_SITE 7
FT ACT_SITE 105
FT ACT_SITE 135
FT ACT_SITE BY SIMILARITY.
SQ SEQUENCE 224 AA; 25394 MW; 3EC2EE2E71B84598 CRC64;

Query Match 53.1%; Score 34; DB 1; Length 224;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 DPLTKLWL 10
DB 173 DPLTKLWL 180

RESULT 96
RNBH2_PYRFU STANDARD; PRT; 224 AA.
AC Q8U036;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease H1 (EC 3.1.26.4) (Rnase H1).
GN RNBH OR PFI1781.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;
DR PIR: A24911; A24911.
DR HSSP: Q28632; 1AN3.
DR InterPro: IPR001400; Somatotropin.

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RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: This enzyme is an endonuclease that degrades the RNA of
CC -1- RNA-DNA hybrids specifically (By similarity).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphomonoester.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the Rnase H1 family.
CC -----
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CC -----
DR EMBL: AE010276; AAL81905.1; -.
DR HAMAP: MF_00052; -.
DR InterPro: IPR001352; Rnase_H1/H11.
DR InterPro: IPR004649; Rnh1.
DR Pfam: PF01351; Rnase_H1; 1.
DR TIGRFAMs: TIGR00729; TIGR00729; 1.
DR HydroLase; Nuclease; Endonuclease; Complete proteome.
FT ACT_SITE 7
FT ACT_SITE 105
FT ACT_SITE 135
FT ACT_SITE BY SIMILARITY.
SQ SEQUENCE 224 AA; 25315 MW; 6A4B686040E323F9 CRC64;

Query Match 53.1%; Score 34; DB 1; Length 224;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 DPLTKLWL 10
DB 173 DPLTKLWL 180

RESULT 97
PRRA_RAT STANDARD; PRT; 227 AA.
AC P09320;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Placental prolactin-like protein A precursor (PUP-A).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278172; PubMed=3755436;
RA Duckworth M.L., Peden L.M., Friesen H.G.;
RT "Isolation of a novel prolactin-like cDNA clone from developing rat
RT placenta."
RL J. Biol. Chem. 261:10879-10884(1986).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: Expressed from days 14 to term of pregnancy.
CC -1- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC -----
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CC -----
DR EMBL: M13750; AAA1890.1; -.
DR PIR: A24911; A24911.
DR HSSP: Q28632; 1AN3.
DR InterPro: IPR001400; Somatotropin.

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DR Pfam; PF00103; hormone; 1.
 DR PROSITE; PS00836; SOMATOTROPIN.
 DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
 DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
 KW Hormone; Placenta; Glycoprotein; Signal.
 FT SIGNAL 1 31
 FT CHAIN 32 227
 FT DISULFID 87 203
 FT DISULFID 220 227
 FT CARBOHYD 41 41
 FT CARBOHYD 175 175
 FT VARIANT 73 73
 SQ SEQUENCE 227 AA; 26387 MW; 159F03A4BDDAD66 CRC64;
 Query Match 53.1%; Score 34; DB 1; Length 227;
 Best Local Similarity 55.6%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 WYDPLTKM 9
 DB 120 WLNPLHLML 128
 RESULT 98
 TRTI_SALTY STANDARD; PRT; 243 AA.
 AC P22107;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Trt complement resistance protein precursor.
 GN TRAT.
 OS Salmoneilla typhimurium.
 OS Plasmid 90 kb virulence.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_Taxid=602;
 RN SEQUENCE FROM N.A.
 RX MEDLINE=90205627; PubMed=2181240;
 RA Sukpovi S., Vuorio R., Qi S.Y., O'Connor D., Rhen M.;
 RT "Characterization of the trt gene and mutants that increase outer
 membrane permeability from the Salmoneilla typhimurium virulence
 plasmid";
 RL Mol. Microbiol. 4:49-57(1990).
 CC -1- FUNCTION: RESPONSIBLE FOR PREVENTING UNPRODUCTIVE CONJUGATION
 BETWEEN BACTERIA CARRYING LIKE PLASMIDS.
 CC -1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
 anchor.
 CC -1- SIMILARITY: STRONG, TO E. COLI TRAT PROTEINS.
 CC -----
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 CC -----
 CC EMBL; X51994; CAA36250.1;
 DR InterPro; IPR000437; Trat_lipoprot_S.
 DR InterPro; IPR008874; Trat.
 DR Pfam; PF05818; Trat; 1.
 KW PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Plasmid; Conjugation; Signal; Lipoprotein; Outer membrane; Palmitate.
 FT SIGNAL 1 20
 FT CHAIN 21 243
 FT LIPID 21 21
 FT LIPID 21 21
 FT SEQUENCE 243 AA; 26278 MW; 27F74BCC71BD385C CRC64;
 Query Match 53.1%; Score 34; DB 1; Length 243;

Best Local Similarity 41.7%; Pred. No. 1.2e+02;
 Matches 5; Conservative 5; Mismatches 0; Indels 2; Gaps 1;
 QY 1 WYDPLTK--LWL 10
 DB 44 WHDPVSERTWVL 55
 RESULT 99
 RNHL_ARATH STANDARD; PRT; 253 AA.
 ID RNHL_ARATH
 AC Q9SEZ6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Probable ribonuclease HI large subunit (EC 3.1.26.-) (RNase HI large
 subunit) (RNase H(35)).
 DE subunit (RNase H(35)).
 GN AT2G25100 OR F13D4.60.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_Taxid=3702;
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana";
 RL Nature 402:761-768(1999).
 CC -1- FUNCTION: Degrades the ribonucleotide moiety on RNA-DNA hybrid
 molecules. Participates in DNA replication (By similarity).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
 phosphomonoester.
 CC -1- SIMILARITY: Belongs to the RNase HII family. Eukaryotic subfamily.
 CC -----
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 CC -----
 CC EMBL; AC018722; AAP19216.1;
 DR PIR; C84644; C84644.
 DR HSSP; O57599; IEKE.
 DR InterPro; IPR001352; RNase_HII/HIII.
 DR Pfam; PF01351; RNase_HII; 1.
 KW Hydrolyase; Nuclease; Endonuclease.
 FT ACT SITE 20
 FT ACT SITE 127
 FT ACT SITE 155
 FT SEQUENCE 253 AA; 28376 MW; A719768DAFEB19C CRC64;
 Query Match 53.1%; Score 34; DB 1; Length 253;
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 DPLTKML 10
 DB 199 DPLTKML 206
 RESULT 100

```

MOBD BPT4
ID MOBD BPT4 STANDARD; PRT; 259 AA.
AC P39241; Q96216;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable mobile endonuclease D.
GN MOBD OR TK-10.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=10665;
RN [1]
RP SEQUENCE FROM N.A.
RA Mzhavia N., Marusich E., Djavakhishvili T., Neitzel J., Peterson S.,
RA Awaya M., Eidemiller J., Canada D., Tracy J., Gailbreath K.,
RA Paddison P., Anderson B., Stidham T., Blattner F., Kutter E.M.;
RT "The 10.7 kb 'nonessential' region of bacteriophage T4 between the
RT genes tk and nrdC: twenty new t4 genes, generally conserved among
RT T-even phages."
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22514363; Pubmed=12626685;
RA Miller E.S., Kutter E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
RT "Bacteriophage T4 genome."
RL Microbiol. Mol. Biol. Rev. 67:86-156 (2003).
CC -1- SIMILARITY: TO PHAGE T4 MOBB AND MOBC.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U76612; AAB26970.1; -.
DR EMBL: AF158101; AAD42592.1; -.
DR InterPro: IPR002711; HNH.
DR InterPro: IPR003615; HNH_nuc.
DR Pfam: PF01844; HNH_1.
DR SMART: SM00507; HNHc; 1.
DR Hydrolase; Nuclease; Endonuclease.
SQ SEQUENCE 259 AA; 30453 MW; C149B7657EA138F4 CRC64;
Query Match 53.1%; Score 34; DB 1; Length 259;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 2 YDPLTKLWL 10
DB 207 YDLTKLWLI 215

```

Search completed: July 12, 2004, 21:27:44
 Job time : 15 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2004, 21:22:37 ; Search time 39 Seconds

(without alignments)
80.902 Million cell updates/sec

Title: US-09-932-613-457

Perfect score: 64

Sequence: 1 WYDPLTKML 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database :
1: sp_bacteria:*
2: sp_fungi:*
3: sp_human:*
4: sp_invertebrate:*
5: sp_mammal:*
6: sp_mhc:*
7: sp_organelle:*
8: sp_phage:*
9: sp_plant:*
10: sp_rickettsia:*
11: sp_virus:*
12: sp_vertebrate:*
13: sp_unclassified:*
14: sp_virus:*
15: sp_bacteria:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	73.4	291	16 Q98F87	Q98F87 rhizobium 1
2	46	71.9	766	6 Q9N1R8	Q9N1R8 ovine aries
3	45	71.9	870	15 Q7SME9	Q7SME9 enzootic na
4	45	70.3	383	10 Q9S102	Q9S102 arabis na
5	45	67.2	482	16 Q9KAO6	Q9KAO6 bacillus ha
6	43	67.2	538	5 Q9VGE5	Q9VGE5 drosophila
7	43	67.2	570	5 Q9VGE5	Q9VGE5 drosophila
8	43	67.2	575	5 Q9VGE5	Q9VGE5 drosophila
9	43	67.2	947	5 Q9VGE5	Q9VGE5 drosophila
10	43	67.2	947	5 Q9VGE5	Q9VGE5 drosophila
11	43	67.2	1218	5 Q9VGE5	Q9VGE5 drosophila
12	42	65.6	119	16 Q98RUI	Q98RUI bradyrhizob
13	42	65.6	176	17 Q98RUI	Q98RUI bradyrhizob
14	42	65.6	227	16 Q98RUI	Q98RUI bradyrhizob
15	42	65.6	290	15 Q9YNA2	Q9YNA2 sheep pulmo
16	42	65.6	291	15 Q9YNA2	Q9YNA2 sheep pulmo

17	42	65.6	293	10 Q94A88	Q94A88 arabis na
18	42	65.6	374	10 Q98178	Q98178 arabis na
19	42	65.6	392	10 Q98178	Q98178 arabis na
20	42	65.6	442	12 Q91H17	Q91H17 discula des
21	42	65.6	619	4 Q9V480	Q9V480 homo sapien
22	42	65.6	641	4 Q9NZX0	Q9NZX0 homo sapien
23	42	65.6	642	4 Q9V6Y0	Q9V6Y0 homo sapien
24	42	65.6	873	6 Q95N65	Q95N65 ovine aries
25	42	65.6	874	15 Q9W673	Q9W673 sheep pulmo
26	41.5	64.8	312	10 Q9AYF3	Q9AYF3 oryza sativ
27	41.5	64.8	312	10 Q9AYF3	Q9AYF3 oryza sativ
28	41.5	64.8	312	10 Q9AYF3	Q9AYF3 oryza sativ
29	41	64.1	144	2 Q9R7Z8	Q9R7Z8 vibrio chol
30	41	64.1	168	2 Q97030	Q97030 vibrio chol
31	41	64.1	309	16 Q98XCI	Q98XCI lactobacill
32	41	64.1	514	10 Q9VMD8	Q9VMD8 lycopersico
33	41	64.1	539	16 Q91V89	Q91V89 bacillus an
34	41	64.1	539	16 Q91V89	Q91V89 bacillus an
35	41	64.1	591	16 Q9VIF7	Q9VIF7 helicobacte
36	41	64.1	604	16 Q9A1Z5	Q9A1Z5 bacteroides
37	41	64.1	655	16 Q9KOR4	Q9KOR4 vibrio chol
38	41	64.1	672	16 Q910K3	Q910K3 pseudomonas
39	41	64.1	694	2 Q91121	Q91121 pseudomonas
40	41	64.1	733	16 Q97U04	Q97U04 rhodospirill
41	41	64.1	808	2 Q97021	Q97021 saccharopol
42	41	64.1	111	9 Q9Y308	Q9Y308 enterobacte
43	41	64.1	173	16 Q97XC5	Q97XC5 pseudomonas
44	41	64.1	230	5 Q917A3	Q917A3 plactyneris
45	41	64.1	345	2 Q99180	Q99180 salmonella
46	41	64.1	345	16 Q93933	Q93933 salmonella
47	41	64.1	378	10 Q9M2B5	Q9M2B5 arabis na
48	41	64.1	500	13 Q970Y2	Q970Y2 xenopus lae
49	41	64.1	513	5 Q9V8N4	Q9V8N4 drosophila
50	41	64.1	519	16 Q9A9X4	Q9A9X4 caulobacter
51	41	64.1	582	4 Q9N5C3	Q9N5C3 homo sapien
52	41	64.1	612	10 Q98B55	Q98B55 oryza sativ
53	41	64.1	612	10 Q98B55	Q98B55 oryza sativ
54	41	64.1	617	5 Q98B51	Q98B51 drosophila
55	41	64.1	620	5 Q91H99	Q91H99 drosophila
56	41	64.1	640	13 Q92VQ8	Q92VQ8 brachydanio
57	41	64.1	648	3 Q92J26	Q92J26 candida alb
58	41	64.1	713	10 Q91M21	Q91M21 oryza sativ
59	41	64.1	715	5 Q91KX0	Q91KX0 plasmodium
60	41	64.1	723	5 Q91KX4	Q91KX4 plasmodium
61	39.5	61.7	283	16 Q977F0	Q977F0 pseudomonas
62	39	60.9	155	2 Q94791	Q94791 rhodobacter
63	39	60.9	155	2 Q94791	Q94791 rhodobacter
64	39	60.9	158	2 Q9RCF8	Q9RCF8 rhodobacter
65	39	60.9	176	2 Q948N8	Q948N8 gamma-prote
66	39	60.9	177	6 Q9GTF8	Q9GTF8 trichosurus
67	39	60.9	240	16 Q9CFP6	Q9CFP6 pasteurilla
68	39	60.9	274	17 Q96YU1	Q96YU1 sulfolobus
69	39	60.9	335	10 Q91Y77	Q91Y77 arabis na
70	39	60.9	365	10 Q97035	Q97035 arabis na
71	39	60.9	403	5 Q9W3D5	Q9W3D5 drosophila
72	39	60.9	430	5 Q91702	Q91702 caenorhabdi
73	39	60.9	440	16 Q97U40	Q97U40 synecococc
74	39	60.9	480	5 Q91700	Q91700 caenorhabdi
75	39	60.9	518	16 Q98G73	Q98G73 pseudomonas
76	39	60.9	551	16 Q94953	Q94953 helicobacte
77	39	60.9	551	16 Q94953	Q94953 helicobacte
78	39	60.9	817	3 Q9HFF8	Q9HFF8 colicystic
79	39	60.9	848	16 Q9A3P6	Q9A3P6 bacteroides
80	39	60.9	871	6 Q9N172	Q9N172 trichosurus
81	39	60.9	941	6 Q97T45	Q97T45 bos taurus
82	39	60.9	948	16 Q98X42	Q98X42 ralestonia s
83	39	60.9	2183	16 Q98585	Q98585 streptomyce
84	38.5	60.2	277	16 Q97U29	Q97U29 rhodospirill
85	38	59.4	33	2 Q91125	Q91125 campylobact
86	38	59.4	43	16 Q98F60	Q98F60 leptospira
87	38	59.4	92	10 Q9W3Q4	Q9W3Q4 silene noct
88	38	59.4	140	16 Q98EUP0	Q98EUP0 mycoplasma
89	38	59.4	190	16 Q9K9C7	Q9K9C7 bacillus ha

90	38	59.4	206	17	027482	027482 methnabact	163	37	57.8	346	10	Q91B96	Q91B96 chlorarachn
91	38	59.4	283	16	Q8A620	Q8A620 bacteroides	164	37	57.8	346	10	Q7X107	Q7X107 chlorarachn
92	38	59.4	295	5	016974	016974 caenothabdi	165	37	57.8	349	2	Q67775	Q67775 xanthomonas
93	38	59.4	300	5	Q9N3X5	Q9N3X5 caenothabdi	166	37	57.8	349	16	Q8P804	Q8P804 xanthomonas
94	38	59.4	302	4	Q81W46	Q81W46 homo sapien	167	37	57.8	355	2	Q91UW6	Q91UW6 escherichia
95	38	59.4	321	3	Q9P3R4	Q9P3R4 neurospora	168	37	57.8	356	16	Q9P0D4	Q9P0D4 ureaplasma
96	38	59.4	341	16	Q91072	Q91072 pseudomonas	169	37	57.8	357	16	Q92ZJ2	Q92ZJ2 rhizobium m
97	38	59.4	345	16	Q8BUT8	Q8BUT8 pseudomonas	170	37	57.8	390	16	Q87CM6	Q87CM6 xyloella fas
98	38	59.4	361	16	Q8BUT8	Q8BUT8 pseudomonas	171	37	57.8	401	16	Q8ACN8	Q8ACN8 caulobacter
99	38	59.4	361	16	Q8BUT8	Q8BUT8 pseudomonas	172	37	57.8	427	13	Q80J26	Q80J26 brachydantio
100	38	59.4	362	10	Q8FXK7	Q8FXK7 bruceella su	173	37	57.8	483	10	Q84LG7	Q84LG7 oryza sativ
101	38	59.4	380	10	Q80573	Q80573 aradidopsis	174	37	57.8	485	5	Q9NA11	Q9NA11 caenothabdi
102	38	59.4	453	11	Q8B280	Q8B280 mus musculu	175	37	57.8	494	5	001965	001965 caenothabdi
103	38	59.4	459	8	Q955T7	Q955T7 cheirogaleu	176	37	57.8	495	4	Q96G42	Q96G42 homo sapien
104	38	59.4	459	8	Q955T7	Q955T7 cheirogaleu	177	37	57.8	505	16	Q96H13	Q96H13 rhizobium 1
105	38	59.4	475	8	Q955T8	Q955T8 cheirogaleu	178	37	57.8	518	16	Q989V7	Q989V7 rhizobium 1
106	38	59.4	475	10	Q9LW55	Q9LW55 aradidopsis	179	37	57.8	536	10	Q947C2	Q947C2 gossypium a
107	38	59.4	485	16	Q8EMQ9	Q8EMQ9 oceanobacti	180	37	57.8	542	5	Q9YVU2	Q9YVU2 dirosophila
108	38	59.4	494	4	Q8N9B9	Q8N9B9 homo sapien	181	37	57.8	573	4	Q43J26	Q43J26 homo sapien
109	38	59.4	503	16	Q8UHS9	Q8UHS9 agrobacteri	182	37	57.8	590	16	Q7UTF4	Q7UTF4 rhodospirell
110	38	59.4	512	10	Q9LV33	Q9LV33 aradidopsis	183	37	57.8	603	16	Q8A878	Q8A878 bacteroides
111	38	59.4	535	11	Q8BUW1	Q8BUW1 mus musculu	184	37	57.8	604	16	Q8A3N2	Q8A3N2 bacteroides
112	38	59.4	549	16	Q24952	Q24952 helicobacte	185	37	57.8	606	16	Q9WXN8	Q9WXN8 bacteroides
113	38	59.4	549	16	Q9ZMU0	Q9ZMU0 helicobacte	186	37	57.8	608	16	Q9X0B2	Q9X0B2 thermotoga
114	38	59.4	558	4	Q8NBB8	Q8NBB8 homo sapien	187	37	57.8	640	11	Q8K430	Q8K430 ratius norv
115	38	59.4	558	11	Q8NBB8	Q8NBB8 mus musculu	188	37	57.8	660	16	Q83055	Q83055 treponema p
116	38	59.4	560	16	Q8PC45	Q8PC45 campylobact	189	37	57.8	663	16	Q8B8U0	Q8B8U0 pseudomonas
117	38	59.4	625	4	Q96SY2	Q96SY2 homo sapien	190	37	57.8	743	8	Q9XQJ7	Q9XQJ7 efylidium c
118	38	59.4	625	5	Q869P8	Q869P8 dictyosteli	191	37	57.8	812	4	Q86VU3	Q86VU3 homo sapien
119	38	59.4	630	16	Q8D7L1	Q8D7L1 vibrio vuln	192	37	57.8	814	16	Q8CW79	Q8CW79 escherichia
120	38	59.4	645	16	Q9RDB4	Q9RDB4 streptomyce	193	37	57.8	839	16	Q8C8C4	Q8C8C4 rhizobium 1
121	38	59.4	728	5	Q9VWZ8	Q9VWZ8 dirosophila	194	37	57.8	952	4	Q8IDU7	Q8IDU7 plasmodium
122	38	59.4	730	16	Q96WS6	Q96WS6 homo sapien	195	37	57.8	965	4	Q8G3C5	Q8G3C5 escherichia
123	38	59.4	734	16	Q8AAM6	Q8AAM6 bacteroides	196	37	57.8	1105	17	Q8FGL0	Q8FGL0 plasmodium
124	38	59.4	779	10	Q93Y21	Q93Y21 aradidopsis	197	37	57.8	1288	17	Q96XW6	Q96XW6 sulfolobus
125	38	59.4	803	17	Q97YH8	Q97YH8 sulfolobus	198	37	57.8	1296	2	Q8VLP4	Q8VLP4 streptococ
126	38	59.4	849	4	Q9NT68	Q9NT68 homo sapien	199	37	57.8	1416	4	Q8TD57	Q8TD57 leishmania
127	38	59.4	888	10	Q81Z25	Q81Z25 aradidopsis	200	37	57.8	222	16	Q9RR69	Q9RR69 delnococtus
128	38	59.4	888	10	Q81Z25	Q81Z25 aradidopsis	201	36.5	57.0	667	16	Q9RJT5	Q9RJT5 streptomyce
129	38	59.4	930	11	Q804C2	Q804C2 mus musculu	202	36.5	57.0	723	12	Q8A279	Q8A279 caulobacter
130	38	59.4	964	4	Q9NV71	Q9NV71 homo sapien	203	36.5	57.0	74	12	Q8VNW2	Q8VNW2 white spot
131	38	59.4	1045	4	Q9NV71	Q9NV71 homo sapien	204	36	56.2	124	10	Q9SKY4	Q9SKY4 oryza sativ
132	38	59.4	1071	4	Q7Z3C7	Q7Z3C7 homo sapien	205	36	56.2	147	16	Q98B12	Q98B12 rhizobium 1
133	38	59.4	1086	4	Q9P2P4	Q9P2P4 mus musculu	206	36	56.2	170	13	Q7ZTW0	Q7ZTW0 brachydantio
134	38	59.4	1198	11	Q8OTF5	Q8OTF5 mus musculu	207	36	56.2	181	8	Q954J6	Q954J6 sarcititrip
135	38	59.4	1769	4	Q9P273	Q9P273 mus musculu	208	36	56.2	181	8	Q954J6	Q954J6 sarcititrip
136	38	59.4	1822	2	Q8VRG6	Q8VRG6 chloroflexu	209	36	56.2	209	11	Q62057	Q62057 listeria mo
137	38	59.4	1828	11	Q80TU2	Q80TU2 mus musculu	210	36	56.2	211	16	Q9X6V2	Q9X6V2 xanthomonas
138	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	211	36	56.2	212	16	Q82V96	Q82V96 xanthomonas
139	38	59.4	2246	11	Q9ULC1	Q9ULC1 mus musculu	212	36	56.2	222	17	Q9UTU6	Q9UTU6 nitrospoma
140	38	59.4	2715	11	Q9WTS6	Q9WTS6 mus musculu	213	36	56.2	232	16	Q7VE68	Q7VE68 methanosarc
141	38	59.4	2765	11	Q9WTS5	Q9WTS5 mus musculu	214	36	56.2	251	10	Q8ASD4	Q8ASD4 oryza sativ
142	38	59.4	2765	11	Q9WTS5	Q9WTS5 mus musculu	215	36	56.2	256	16	Q8EYQ3	Q8EYQ3 mycoplasma
143	38	59.4	2771	11	Q9R1K2	Q9R1K2 ractus norv	216	36	56.2	264	17	Q8EYQ3	Q8EYQ3 mycoplasma
144	38	59.4	2771	11	Q9WTS7	Q9WTS7 mus musculu	217	36	56.2	284	12	Q71105	Q71105 bovine aden
145	38	59.4	2802	13	Q9DERS	Q9DERS mus musculu	218	36	56.2	310	11	Q8C6R9	Q8C6R9 neurospora
146	38	59.4	2825	11	Q70465	Q70465 mus musculu	219	36	56.2	311	16	Q888J1	Q888J1 lacticobacilli
147	38	59.4	2825	11	Q70465	Q70465 mus musculu	220	36	56.2	311	16	Q888J1	Q888J1 lacticobacilli
148	38	59.4	227	16	Q92515	Q92515 mycobacteri	221	36	56.2	321	2	Q93R45	Q93R45 thermus the
149	38	59.4	227	16	Q92515	Q92515 mycobacteri	222	36	56.2	321	2	Q93R45	Q93R45 thermus the
150	38	59.4	227	16	Q92515	Q92515 mycobacteri	223	36	56.2	321	2	Q93R45	Q93R45 thermus the
151	38	59.4	227	16	Q92515	Q92515 mycobacteri	224	36	56.2	321	2	Q93R45	Q93R45 thermus the
152	38	59.4	227	16	Q92515	Q92515 mycobacteri	225	36	56.2	321	2	Q93R45	Q93R45 thermus the
153	38	59.4	227	16	Q92515	Q92515 mycobacteri	226	36	56.2	321	2	Q93R45	Q93R45 thermus the
154	38	59.4	227	16	Q92515	Q92515 mycobacteri	227	36	56.2	321	2	Q93R45	Q93R45 thermus the
155	38	59.4	227	16	Q92515	Q92515 mycobacteri	228	36	56.2	321	2	Q93R45	Q93R45 thermus the
156	38	59.4	227	16	Q92515	Q92515 mycobacteri	229	36	56.2	321	2	Q93R45	Q93R45 thermus the
157	38	59.4	227	16	Q92515	Q92515 mycobacteri	230	36	56.2	321	2	Q93R45	Q93R45 thermus the
158	38	59.4	227	16	Q92515	Q92515 mycobacteri	231	36	56.2	321	2	Q93R45	Q93R45 thermus the
159	38	59.4	227	16	Q92515	Q92515 mycobacteri	232	36	56.2	321	2	Q93R45	Q93R45 thermus the
160	38	59.4	227	16	Q92515	Q92515 mycobacteri	233	36	56.2	321	2	Q93R45	Q93R45 thermus the
161	38	59.4	227	16	Q92515	Q92515 mycobacteri	234	36	56.2	321	2	Q93R45	Q93R45 thermus the
162	38	59.4	227	16	Q92515	Q92515 mycobacteri	235	36	56.2	321	2	Q93R45	Q93R45 thermus the

236	36	56.2	375	11	09CY38	09CY38 mus musculus
237	36	56.2	379	13	09NK28	09NK28 eptaretus
238	36	56.2	380	17	08TKX0	08TKX0 methanosarc
239	36	56.2	405	16	09PCF3	09PCF3 xylella fas
240	36	56.2	411	16	07VAS8	07VAS8 prochloroco
241	36	56.2	413	16	083208	083208 enterococu
242	36	56.2	416	11	0805V4	0805V4 mus musculu
243	36	56.2	418	10	08L991	08L991 arabidopsis
244	36	56.2	418	10	09M1Y1	09M1Y1 arabidopsis
245	36	56.2	419	2	046445	046445 chlamydia t
246	36	56.2	423	11	08BTG8	08BTG8 mus musculu
247	36	56.2	424	16	084654	084654 chlamydia t
248	36	56.2	427	16	083185	083185 shigella fl
249	36	56.2	429	11	08BS99	08BS99 mus musculu
250	36	56.2	432	16	0839E4	0839E4 enterococu
251	36	56.2	445	11	08CFJ4	08CFJ4 mus musculu
252	36	56.2	451	16	08FCF1	08FCF1 escherichia
253	36	56.2	459	8	09G3S7	09G3S7 pteropus sc
254	36	56.2	459	8	09G6M6	09G6M6 pteropus da
255	36	56.2	460	16	09PH40	09PH40 xylella fas
256	36	56.2	460	16	087E57	087E57 xylella fas
257	36	56.2	472	16	088QJ3	088QJ3 pseudomonas
258	36	56.2	473	3	08J0B2	08J0B2 neotrypanid
259	36	56.2	476	11	09R0J8	09R0J8 mus musculu
260	36	56.2	485	11	08BTM6	08BTM6 mus musculu
261	36	56.2	493	2	08GE77	08GE77 streptomyce
262	36	56.2	516	10	07XYP6	07XYP6 oryza sativ
263	36	56.2	531	5	0966P6	0966P6 caenorhabdi
264	36	56.2	531	5	061795	061795 caenorhabdi
265	36	56.2	540	5	P90787	P90787 caenorhabdi
266	36	56.2	571	11	09CR40	09CR40 mus musculu
267	36	56.2	589	13	07ZUX7	07ZUX7 xenopus lae
268	36	56.2	620	4	07Z330	07Z330 homo sapien
269	36	56.2	629	11	08C1U1	08C1U1 mus musculu
270	36	56.2	629	11	08CD84	08CD84 mus musculu
271	36	56.2	642	10	09S944	09S944 vitis vinif
272	36	56.2	642	11	099KN0	099KN0 mus musculu
273	36	56.2	642	11	092008	092008 mus musculu
274	36	56.2	652	5	081427	081427 plasmodium
275	36	56.2	654	11	08C706	08C706 mus musculu
276	36	56.2	691	11	08C7K3	08C7K3 sarcophaga
277	36	56.2	713	5	09GV24	09GV24 sarcophaga
278	36	56.2	726	8	08HTM9	08HTM9 sinopodophy
279	36	56.2	726	8	08HTM8	08HTM8 diphyllaia
280	36	56.2	726	8	08HTM7	08HTM7 podophyllum
281	36	56.2	726	8	08HTM6	08HTM6 dysosma ple
282	36	56.2	728	16	08YMT0	08YMT0 arabidopsis
283	36	56.2	756	5	061224	061224 scypha raph
284	36	56.2	795	10	08LOJ1	08LOJ1 oryza sativ
285	36	56.2	795	17	08J2W5	08J2W5 pyrococcus
286	36	56.2	806	4	09FNA3	09FNA3 arabidopsis
287	36	56.2	808	4	09UFX3	09UFX3 homo sapien
288	36	56.2	954	4	096AY1	096AY1 homo sapien
289	36	56.2	954	4	09UI93	09UI93 homo sapien
290	36	56.2	954	4	09NZC9	09NZC9 homo sapien
291	36	56.2	1033	11	08K137	08K137 mus musculu
292	36	56.2	1036	11	08BW12	08BW12 mus musculu
293	36	56.2	1148	3	003897	003897 saccharomyc
294	36	56.2	1223	12	09INJ2	09INJ2 kadipiro vi
295	36	56.2	1249	12	065152	065152 african swi
296	36	56.2	1269	17	097206	097206 sulfobus
297	36	56.2	1292	3	09C163	09C163 rhizomucor
298	36	56.2	1328	4	08CHS5	08CHS5 mus musculu
299	36	56.2	1398	4	014997	014997 homo sapien
300	36	56.2	1803	11	09ESY1	09ESY1 rattus norv

ALIGNMENTS

RESULT 1
098FS7
ID 098FS7
PRELIMINARY: PRT: 291 AA.

AC	098FS7:	Query Match	73.4%	Score 47;	DB 16;	Length 291;
DT	01-OCT-2001 (TRENBLREL. 18, Created)	Best Local Similarity	70.0%	Pred. No. 5.8;		
DT	01-OCT-2001 (TRENBLREL. 18, Last sequence update)	Matches	7;	Conservative	1;	Mismatches 2; Indels 0; Gaps 0;
DE	01-MAR-2002 (TRENBLREL. 20, Last annotation update)					
DE	Hypothetical protein mlr3636.					
GN	MLR3636.					
OS	Rhizobium loti (Mesorhizobium loti).					
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;					
OC	Phyllobacteriaceae; Mesorhizobium.					
OX	NCBI_TaxID=381;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=MAFF03039;					
RX	MEDLINE=21082930; PubMed=11214968;					
RA	Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,					
RA	Watanabe A., Idekawa K., Ishikawa A., Kawashima K., Kimura T.,					
RA	Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,					
RA	Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,					
RA	Takeuchi C., Yamada M., Tabata S.;					
RT	"Complete genome structure of the nitrogen-fixing symbiotic bacterium					
RT	Mesorhizobium loti."					
RL	DNA Res. 7:331-338(2000).					
DR	EMBL; AP003002; BAB50490.1;					
KW	Hypothetical protein; Complete proteome.					
SK	SEQUENCE 291 AA; 31162 MW; 36E651E33A79E82 CRC64;					
QY	1 MYDPLTKLWL 10					
DB	22 WFAPLTSLWL 31					
RESULT 2						
ID	09NIR8	PRELIMINARY:	PRT:	766 AA.		
AC	09NIR8:					
DT	01-OCT-2000 (TRENBLREL. 15, Created)					
DT	01-OCT-2000 (TRENBLREL. 15, Last sequence update)					
DT	01-OCT-2003 (TRENBLREL. 25, Last annotation update)					
GN	Pol.					
OS	Ovis aries (sheep).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;					
OC	Bovidae; Caprinae; Ovis.					
OX	NCBI_TaxID=9940;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=20392162; PubMed=10933716;					
RA	Palmarini M., Halliworth C., York D., Murgia C., de Oliveira T.,					
RA	Spencer T., Fan H.;					
RT	"Molecular cloning and functional analysis of three type D endogenous					
RT	retroviruses of sheep reveal a different cell tropism from that of the					
RT	highly related exogenous Jaagsiekte sheep retrovirus."					
RL	J. Virol. 74:8065-8076(2000).					
DR	EMBL; AF153615; AAF29458.1;					
DR	GO; GO:0003677; F:DNA binding; IEA.					
DR	GO; GO:0008907; F:integrase activity; IEA.					
DR	GO; GO:0004523; F:ribonuclease H activity; IEA.					
DR	GO; GO:0003723; F:RNA binding; IEA.					
DR	GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.					
DR	GO; GO:0008270; F:transferase activity; IEA.					
DR	GO; GO:0005074; F:zinc ion binding; IEA.					
DR	GO; GO:0006310; P:DNA integration; IEA.					
DR	GO; GO:0006278; P:RNA dependent DNA replication; IEA.					
DR	InterPro; IPR001037; Integrase_C.					
DR	InterPro; IPR003308; Integrase_Zn.					
DR	InterPro; IPR002156; RNaseH.					
DR	InterPro; IPR001584; Rve.					

DR InterPro: IPR000477; RVTse.
 DR Pfam: PF002022; Integrase_2n; 1.
 DR Pfam: PF000075; rnaaseh; 1.
 DR Pfam: PF00665; rve; 1.
 DR Pfam: PF00078; rvc; 1.
 DR RNA-directed DNA polymerase; Transferase.
 SQ SEQUENCE 766 AA; 86948 MW; 0CC13CCBED56BE99 CRC64;

Query Match
 Best Local Similarity 71.9%; Score 46; DB 6; length 766;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
 DB 720 WKDPLTKLW 728

RESULT 3
 07SME9 PRELIMINARY; PRT; 870 AA.
 AC 07SME9; PRELIMINARY; PRT; 870 AA.
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, last sequence update)
 DE Gag-pro-pol fusion (fragment).
 OS Enzootic nasal tumour virus of goats.
 OC Viruses; Retroviridae; Retroviridae; Betaretrovirus.
 NCBI_TaxID=339365;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22749839; PubMed=12867657;
 RA Orlin A., Couzens C., Minguion E., Pascual Z., Villarreal M.P.,
 RT Sharp J.M., Heras Mde L.,
 RT "Characterization of enzootic nasal tumour virus of goats: complete
 RT sequence and tissue distribution."
 RL J. Gen. Virol. 84:2245-2252 (2003).
 DR EMBL, AY197548; AAC05306.2; -.
 FT NON TER 1
 SQ SEQUENCE 870 AA; 99214 MW; 346D1642CDA4C3D4 CRC64;

Query Match
 Best Local Similarity 71.9%; Score 46; DB 15; length 870;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
 DB 813 WKDPLTKLW 821

RESULT 4
 09S102 PRELIMINARY; PRT; 383 AA.
 AC 09S102; PRELIMINARY; PRT; 383 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, last annotation update)
 DE A2322030 protein (Hypothetical protein).
 GN A2322030.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., Vanaken S.E., Unayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana."
 RL Nature 402:761-768 (1999).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RN Lin X.;
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RN Lin X.;
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,
 RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
 RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
 RA Fraser C.M., Venter J.C.;
 RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DL EMBL, AC007232; AAD25821.1; -.
 DR EMBL, AC007019; AAM15347.1; -.
 DR PIR, B84608; B84608.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR006552; Kelch_rep.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF01344; Kelch; 3.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00612; Kelch; 2.
 SQ SEQUENCE 383 AA; 43474 MW; 23C6E99C913FED71 CRC64;

Query Match
 Best Local Similarity 70.3%; Score 45; DB 10; length 383;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
 DB 288 WYDPLTKLW 296

RESULT 5
 09KA06 PRELIMINARY; PRT; 482 AA.
 ID 09KA06; PRELIMINARY; PRT; 482 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, last annotation update)
 DE Hypothetical protein BH2231.
 GN BH2231.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kihara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis."
 RL Nucleic Acids Res. 28:4317-4331 (2000).
 DR EMBL, AP001514; BAB05950.1; -.
 DR PIR, G83928; G83928.
 DR InterPro: IPR001173; Glyco_trans 2.
 DR Pfam: PF00535; Glycos_transf 2; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 482 AA; 54881 MW; CFI51B8CF8982AD CRC64;

Query Match
 Best Local Similarity 70.3%; Score 45; DB 16; length 482;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
 DB 111 WYDPLTKLW 111

DB 443 WYRLTVLM 451

RESULT 6

ID Q9VGE6 PRELIMINARY; PRT; 538 AA.

AC Q9VGE6; MEDLINE=20196006; PubMed=10731132.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE CG3571 protein.

GN CG3571.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley;

RX MEDLINE=20196006; PubMed=10731132.

RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baker E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Bokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,

RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Fogel A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jajalil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Mezuklov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kimios I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL EMBL; AB003694; AAF54738.1; -

DR GO; GO:0005315; F:Protein binding; IEA.

DR InterPro; IPR000210; BTB_POZ.

DR InterPro; IPR006521; Kelch_rep.

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9

DB 275 YDPLTKSM 282

RESULT 7

ID 017698 PRELIMINARY; PRT; 570 AA.

AC 017698; MEDLINE=99069613; PubMed=9851916;

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE C53A5.6 protein.

GN C53A5.6.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Peloderiinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley;

RX MEDLINE=99069613; PubMed=9851916;

RA Mortimore B.J.;

RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley;

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RA "Genome sequence of the nematode C. elegans: A platform for

RT investigating biology.";

RL Science 282:2012-2018 (1998).

CC -1. SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL; Z81486; CAB03987.1; -

DR PIR; T20166; T20166.

DR WormPep; C53A5.6; CE08955.

DR InterPro; IPR006521; Kelch.

DR InterPro; IPR006522; Kelch_rep.

DR InterPro; IPR001841; Znf_fing.

DR Pfam; PF01344; Kelch; 6.

DR Pfam; PF00097; ZF-C3HC4; 1.

DR PRINTS; PR00501; KELCHREPEAT.

DR SMART; SM00612; Kelch; 4.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS50089; ZF_RING_2; 1.

DR Metal-binding; Zinc; Zinc-finger.

SQ SEQUENCE 570 AA; 63294 MW; 58B5E1BE24FBA0F5 CRC64;

Query Match 67.2%; Score 43; DB 5; Length 570;

Best Local Similarity 87.5%; Pred. No. 54;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9

DB 492 YDPLTKSM 499

RESULT 8

ID Q9VGE5 PRELIMINARY; PRT; 575 AA.

AC Q9VGE5; MEDLINE=20196006; PubMed=10731132.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE CG3571 protein (LD42169P).

GN CG3571.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley;

ULT 9
 YAL
 Q8SYAL
 PRELIMINARY;
 PRT; 947 AA

MEDLINE@csikereley;
 PAdams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 Sutton G.G., Lewis S.R., Richards S., Ashburner M., Henderson S.,
 Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blasey K.G., Chame M., Peiffer B.

Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Abilil J.F., Agbayanti A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale U., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svrtkase R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang X., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 "The genome sequence of *Drosophila melanogaster*,"
 Science 287:2185-2195(2000).

[12]

SEQUENCE FROM N.A.
 RP Celniker S.E., Adams M.D., Krommiller B., Man K.H., Holt R.A.,
 Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 Barzon J., An H., Baldwin D., Barzon J., Beeson K.Y., Busam D.A.,
 Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 Fierliera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 Stapleton M., Strong R., Svrtkase R., Tector C., Tyler D.,
 Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
 "Sequencing of *Drosophila melanogaster* genome,"
 Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 [13]
 RP SEQUENCE FROM N.A.
 RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,
 Hirdecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 Tuoy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
 Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield D.,
 Asburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 "Annotation of *Drosophila melanogaster* genome,"
 Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 [14]
 RP SEQUENCE FROM N.A.
 RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,
 Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 [15]
 RP SEQUENCE FROM N.A.
 RP Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AE003796; AAM70845.1; -
 DR FLYBase: FBgn0034421; CG7097.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO: GO:0005083; F:small GTPase regulatory/interacting protein. . .; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR001180; Citron.
 DR InterPro: IPR000719; Prot. kinase.
 DR InterPro: IPR002290; Ser. Thr. kinase.
 DR InterPro: IPR001245; Tyr. kinase.
 DR Pfam: PF00780; CNH; 1.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot. kinase; 1.
 DR SMART: SM00036; CNH; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR SMART: SM00219; TYK; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
 DR ATP-binding; Transferrase.
 DR SEQUENCE 947 AA; 105195 MW; 480EC8A8AE0D0E0 CRC64;
 Query Match 67.2%; Score 43; DB 5; Length 947;
 Best Local Similarity 70.0%; Pred. No. 89;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Db 729 WYDPLKXML 738
 1 WYDPLKXML 10
 |||||
 729 WYDPLKXML 738
 RESULT 11
 Q9VBR6 PRELIMINARY; PRT; 1218 AA.
 ID Q9VBR6
 AC Q9VBR6
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CG7097 protein.
 GN CG7097
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Abilil J.F., Agbayanti A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.A., Bouck J., Brokstein P., Broctier P.,
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskye R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Maassman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003796; AAF57593.1; -.
 DR HSSP: Q63450; 1A06.
 DR FLYbase; FBgn0034421; CG7097.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0005083; F:small GTPase regulatory/interacting protein. . ; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR001180; CItrom.
 DR InterPro: IPR000719; Prot_kinase.
 DR Pfam: PF00780; CNH; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART; SM00036; CNH; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR ATP-binding; Transferase
 SQ SEQUENCE 1218 AA; 132395 MW; 7847FAFP80CEDC8 CRC64;
 Query Match 67.2%; Score 43; DB 5; Length 1218;
 Best Local Similarity 70.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 WYDPLTKLWL 10
 Db 1000 WYDPLTKLWL 1009

RESULT 12
 Q89RUI PRELIMINARY; PRT; 119 AA.
 AC Q89RUI;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE BLR2671 protein.
 GN BLR2671.
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiales; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA 110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Ideawa K., Iitiguchi M., Kawashima K.,
 RA Kohara M., Matsunoto M., Shimo S., Tsurunaka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197(2002).
 DR EMBL: AP005944; BAC47936.1; -.
 DR Complete proteome.
 KW SEQUENCE 119 AA; 13303 MW; 799D98A891244914 CRC64;
 Query Match 65.6%; Score 42; DB 16; Length 119;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 Db 71 WYDPLTKLWL 80

RESULT 13
 Q8TP13 PRELIMINARY; PRT; 176 AA.
 AC Q8TP13;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Predicted protein.
 GN MA2114.
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=11932238;
 RA Galagan J.E., Nusbaum C., Koy A., Endrizzi M.G., MacDonald P.,
 RA Fitzhugh W., Galvo S., Engels R., Smirnov S., Ancoor D., Brown A.,
 RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
 RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
 RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.W., Birren B.;
 RT "The genome of *Methanosarcina acetivorans* reveals extensive metabolic
 and physiological diversity.";
 RL Genome Res. 12:532-542(2002).
 DR EMBL: AE010898; AAM05512.1; -.
 DR InterPro: IPR007404; DUF457.
 DR Pfam: PF04307; DUF457; 1.
 KW Complete proteome.
 SQ SEQUENCE 176 AA; 20158 MW; 6E257BDCA71F2027 CRC64;
 Query Match 65.6%; Score 42; DB 17; Length 176;
 Best Local Similarity 66.7%; Pred. No. 25;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WYDPLTKLWL 9
 Db 105 WYDPLTKLWL 113

RESULT 14
 Q7VRS7 PRELIMINARY; PRT; 227 AA.
 AC Q7VRS7;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Putative urease accessory protein F.
 GN UREB OR BRL522.
 OS Candidatus Blochmannia floridanus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
 OX NCBI_TaxID=203907;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22784745; PubMed=12886019;
 RX Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candela F.,
 RA Latorre A., Rausell C., Kamerbeek J., Gadau J., Hoellhobler B.,
 RA van Ham R.C.H.J., Gross R., Moya A.;
 RT "The genome sequence of *Blochmannia floridanus*: comparative analysis
 of reduced genomes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).

DR EMBL: BX248586; CAD83208.1; -
 KW Complete Proteome.
 SQ SEQUENCE 227 AA; 26407 MW; 0A1B45979F9BC1B0 CRC64;

Query Match 65.6%; Score 42; DB 16; Length 227;
 Best Local Similarity 55.6%; Pred. No. 32;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9
 DB 116 WYDPLSDSW 124

RESULT 15

O9YNA2 PRELIMINARY; PRT; 290 AA.

ID O9YNA2
 AC O9YNA2
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Reverse transcriptase (Fragment).
 GN GAG-POL OR POL.
 OS Sheep pulmonary adenomatosis virus (Jaagsiekte sheep retrovirus)
 OS (JSRV).
 OC Viruses; Retrovirus; Retroviridae; Betaretrovirus.
 OX NCBI_TaxID=11746;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JST;
 RX MEDLINE=99296727; PubMed=10366570;
 RA Bai J., Bishop J.V., Carlson J.O., Demartini J.C.;
 RT "Sequence comparison of JSRV with endogenous proviruses: envelope
 RT receptor." and a novel ORF with similarity to a G-protein-coupled
 RT receptor."
 RL Virology 258:333-343(1999).
 CC -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
 CC (BY SIMILARITY).
 DR EMBL: Y18301; CAA7113.1; -
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR GO: GO:0004519; F:endonuclease activity; IEA.
 DR GO: GO:0016787; F:hydrolyase activity; IEA.
 DR GO: GO:0008907; F:integrase activity; IEA.
 DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0015074; P:DNA integration; IEA.
 DR GO: GO:0006310; P:DNA recombination; IEA.
 DR InterPro: IPR001037; Integrase_C.
 DR InterPro: IPR003308; Integrase_Zn.
 DR Pfam: PF00552; Integrase_1.
 DR Pfam: PF02022; Integrase_Zn; 1.
 DR Pfam: PF00655; Ite; 1.
 KW Endonuclease; Hydrolyase; Nucleotidyltransferase; Polyprotein;
 KW RNA-directed DNA polymerase; Transferase.
 FT NON TER 1
 SQ SEQUENCE 290 AA; 33190 MW; C33D2BD840222210 CRC64;

Query Match 65.6%; Score 42; DB 15; Length 290;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9
 DB 229 WKDPTNLW 237

RESULT 16

O9YNA2 PRELIMINARY; PRT; 291 AA.

ID O9YNA2
 AC O9YNA2
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Reverse transcriptase (Fragment).
 GN GAG-POL OR POL.
 OS Sheep pulmonary adenomatosis virus (Jaagsiekte sheep retrovirus)
 OS (JSRV).
 OC Viruses; Retrovirus; Retroviridae; Betaretrovirus.
 OX NCBI_TaxID=11746;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=83RS28;
 RX MEDLINE=99296727; PubMed=10366570;
 RA Bai J., Bishop J.V., Carlson J.O., Demartini J.C.;
 RT "Sequence comparison of JSRV with endogenous proviruses: envelope
 RT receptor." and a novel ORF with similarity to a G-protein-coupled
 RT receptor."
 RL Virology 258:333-343(1999).
 CC -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
 CC (BY SIMILARITY).
 DR EMBL: Y18303; CAA7117.1; -
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR GO: GO:0004519; F:endonuclease activity; IEA.
 DR GO: GO:0016787; F:hydrolyase activity; IEA.
 DR GO: GO:0008907; F:integrase activity; IEA.
 DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0015074; P:DNA integration; IEA.
 DR GO: GO:0006310; P:DNA recombination; IEA.
 DR InterPro: IPR001037; Integrase_C.
 DR InterPro: IPR003308; Integrase_Zn.
 DR Pfam: PF00552; Integrase_1.
 DR Pfam: PF02022; Integrase_Zn; 1.
 DR Pfam: PF00655; Ite; 1.
 KW Endonuclease; Hydrolyase; Nucleotidyltransferase; Polyprotein;
 KW RNA-directed DNA polymerase; Transferase.
 FT NON TER 1
 SQ SEQUENCE 291 AA; 33372 MW; 34912961BDEDF4B CRC64;

Query Match 65.6%; Score 42; DB 15; Length 291;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9
 DB 230 WKDPTNLW 238

RESULT 17

O49488 PRELIMINARY; PRT; 293 AA.

ID O49488
 AC O49488
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN F28A23.70 OR ATG34170.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Weichselgartner M., Fartmann B., Grandérath K., Dauner D.,
 RA Herzl A., Neumann S., Hobeisel J., Jesse T., Heijnen L., Vos P.,
 RA Mewes H.W., Mayer K., Schueller C.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Weichselgartner M., Fartmann B., Grandérath K., Dauner D., Herzl A.,
 RA Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL021961; CAA17555.1; -
DR EMBL; AL161585; CAB80134.1; -
DR PIR; T05419; T05419.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR006652; Kelch_rep.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF01344; Kelch; 2.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00612; Kelch; 2.
KW Hypothetical protein.
SQ SEQUENCE 293 AA; 33448 MW; 5049260E16880E CRC64;
Query Match 65.6%; Score 42; DB 10; Length 293;
Best Local Similarity 55.6%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
CY 1 WYDPLTKLM 9
DB 244 WYDPERRW 252
RESULT 18
ID 081798 PRELIMINARY; PRT; 374 AA.
AC 081798;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Putative polygalacturonase (Fragment).
GN P8D20.180 OR AT4G35670.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Koester P., Hempel S., Entian K.-D., Hohnel J., Jesse T.,
RA Heinen L., Vos P., Mewes H.W., Mayer K.F.X., Scheller C., Bevan M.,
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.,
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
(POLYGLACTURONASES).
DR EMBL; AL031135; CAA20037.1; -
DR EMBL; AL161587; CAB80283.1; -
DR PIR; B85421; B85421.
DR PIR; T04672; T04672.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0004650; F:polygalacturonase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR00743; Glyco_hydro_28.
DR InterPro; IPR006626; Pfh1.
DR Pfam; PF00295; Glyco_hydro_28; 1.
DR SMART; SM00710; Pfh1; 5.
DR PROSITE; PS00502; POLYGLACTURONASE; 1.
KW Cell wall; Glycosidase; Hydrolase; Signal.
FT NON TER 1
SQ SEQUENCE 374 AA; 39884 MW; 3B86DB19DFB1ACB9 CRC64;
Query Match 65.6%; Score 42; DB 10; Length 374;
Best Local Similarity 40.0%; Pred. No. 52;

Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
CY 1 WYDPLTKLM 10
DB 91 WSDPISRMWT 100
RESULT 19
ID Q95VA3 PRELIMINARY; PRT; 392 AA.
AC Q95VA3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein (At4G39550).
GN F23K16.180 OR AT4G39550.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Beyer M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Beyer M., Murphy G., Ridley P., Lemcke K., Scheller C.,
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.,
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Shun P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,
RA Chan W.M., Chang C.H., Dale J.M., Hayashizaki Y., Huan V.W.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
RT "Arabidopsis ORF clones."
RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL078620; CAB44690.1; -
DR EMBL; AL161595; CAB80618.1; -
DR EMBL; BT003146; AAC24578.1; -
DR PIR; T09371; T09371.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR006652; Kelch_rep.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF01344; Kelch; 2.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00612; Kelch; 2.
KW Hypothetical protein.
SQ SEQUENCE 392 AA; 44269 MW; 1EE507551D61FB7B CRC64;
Query Match 65.6%; Score 42; DB 10; Length 392;
Best Local Similarity 55.6%; Pred. No. 55;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
CY 1 WYDPLTKLM 9
DB 297 WYDTMARLM 305
RESULT 20
Q91HT7

ID Q91H17 PRELIMINARY; PRT; 442 AA.
AC Q91H17;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Capsid protein.
OS Discula destructiva virus 2.
OC Viruses; dsRNA viruses; Partitiviridae; Partitivirus.
NCBI_TaxID=160484;
RN NCBI_TaxID=160484;
RP SEQUENCE FROM N.A.
RC STRAIN=331;
RA Rong R., Scott S.W., Rao S., Garner G.R., Tainter F.H.;
RT "Cloning and sequencing of dsRNAs of a previously unreported virus
found in Discula destructiva".
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY033437; AAK59380.1; -
SQ SEQUENCE 442 AA; 47916 MW; 81A5405361AB6979 CRC64;
Query Match 65.6%; Score 42; DB 12; Length 442;
Best Local Similarity 60.0%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 YDPLTKLM 10
Db 212 WKPEPLRLML 221
RESULT 21
Q9Y480 PRELIMINARY; PRT; 619 AA.
AC Q9Y480;
DT 01-NOV-1999 (TRENBLREL. 12, Created)
DT 01-NOV-1999 (TRENBLREL. 12, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE NS1-binding protein.
GN NS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=98362120; PubMed=9696811;
RA Wolff T., O'Neill R.B., Palese P.;
RT "NS1-binding protein (NS1-BP): a novel human protein that interacts
with the influenza A virus nonstructural NS1 protein is relocalized in
the nuclei of infected cells".
RL J. Virol. 72:7170-7180(1998).
DR EMBL; AJ012449; CAA10029.1; -
DR HSSP; Q05516; ICS3.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR006651; Kelch.
DR InterPro; IPR006652; Kelch_rep.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF01344; Kelch; 6.
DR PRINTS; PR00501; KELCHREPEAT.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00612; Kelch; 5.
DR PROSITE; PS50097; BTB; 1.
SQ SEQUENCE 619 AA; 69032 MW; 5CFF8F5F2735DBA CRC64;
Query Match 65.6%; Score 42; DB 4; Length 619;
Best Local Similarity 75.0%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 YDPLTKLM 9
Db 485 FDPVTKLM 492
RESULT 22

Q9NZX0 PRELIMINARY; PRT; 641 AA.
ID Q9NZX0
AC Q9NZX0;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE HSPC068.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=20493367; PubMed=11042152;
RA Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,
RA Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,
RA Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;
RT "Cloning and functional analysis of cDNAs with open reading frames for
300 previously undefined genes expressed in CD34+ hematopoietic
stem/progenitor cells".
RL Genome Res. 10:1546-1560(2000).
DR EMBL; AF161553; AAF29040.1; -
DR HSSP; Q05516; ICS3.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR006651; Kelch.
DR InterPro; IPR006652; Kelch_rep.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF01344; Kelch; 6.
DR PRINTS; PR00501; KELCHREPEAT.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00612; Kelch; 5.
DR PROSITE; PS50097; BTB; 1.
SQ SEQUENCE 641 AA; 71605 MW; B7451584FC79C87A CRC64;
Query Match 65.6%; Score 42; DB 4; Length 641;
Best Local Similarity 75.0%; Pred. No. 89;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 YDPLTKLM 9
Db 484 FDPVTKLM 491
RESULT 23
Q9Y6Y0 PRELIMINARY; PRT; 642 AA.
AC Q9Y6Y0;
DT 01-NOV-1999 (TRENBLREL. 12, Created)
DT 01-NOV-1999 (TRENBLREL. 12, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Hypothetical protein KIAA0850 (NS1-binding protein-like protein).
GN KIAA0850.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosewa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro".
RL DNA Res. 5:355-364(1998).
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC Chen B.S., Zhang K.M.;
RA "A novel gene from endothelium cells stimulated by human plasma
LDL-similar to NS1-binding protein".

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB020657; BAA74873.1; -
DR EMBL: AF205218; AAG43485.1; -
DR HSP: Q05516; ICS3.
DR Genew: HGNC:16951; IVNS1ABP.
DR GO: GO:0005681; C:spliceosome complex; TAS.
DR GO: GO:0005667; C:transcription factor complex; TAS.
DR GO: GO:0006371; P:mRNA splicing; TAS.
DR GO: GO:0009615; P:response to viruses; TAS.
DR InterPro: IPR00210; BTB_POZ.
DR InterPro: IPR006651; Kelch.
DR Pfam: PF00651; BTB_1.
DR Pfam: PF01344; Kelch_6.
DR PRINTS: PRO0501; KELCHREPEAT.
DR SMART: SM00225; BTB_1.
DR PROSITE: PS50097; BTB_1.
KM Hypothetical protein.
SQ SEQUENCE 642 AA; 71729 MW; 456530DC4E351CCD CRC64;

Query Match 65.6%; Score 42; DB 4; Length 642;
Best Local Similarity 75.0%; Pred. No. 89;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YDPLTKLW 9
Db 485 FDPVTKLW 492

RESULT 24
ID Q95N66 PRELIMINARY; PRT; 873 AA.
AC Q95N66;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polymerase (Fragment).
GN POL.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184705; PubMed=11287573;
RA DeMartini J.C., Bishop J.V., Allen T.E., Jassim F.A., Sharp J.M.,
de las Heras M., Voelker D.R., Carlson J.O.;
RT "Jaagsiekte Sheep Retrovirus Proviral Clone JSRV(JS7) , Derived from
RT the JS7 Lung Tumor Cell line, Induces Ovine Pulmonary Carcinoma and Is
RT Integrated into the Surfactant Protein A Gene.",
RL J. Virol. 75:4239-4246(2001).
DR EMBL: AF357971; AAK38686.1; -
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0008907; F:integrase activity; IEA.
DR GO: GO:0004523; F:ribonuclease H activity; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0015074; F:DNA integration; IEA.
DR GO: GO:0006310; P:DNA recombination; IEA.
DR GO: GO:0006278; P:RNA dependent DNA replication; IEA.
DR InterPro: IPR001037; Integrase_C.
DR InterPro: IPR003308; Integrase_Zn.
DR InterPro: IPR002156; RNaseH.
DR InterPro: IPR001584; Rve.
DR InterPro: IPR000477; RVTse.
DR Pfam: PF00552; Integrase_1.
DR Pfam: PF02022; Integrase_Zn_1.
DR Pfam: PF00075; RNaseH_1.
SQ SEQUENCE 874 AA; 99701 MW; 85AC1ADE4DB97DB8 CRC64;

Query Match 65.6%; Score 42; DB 15; Length 874;

DR Pfam: PF00665; Ive; 1.
DR Pfam: PF00078; Ivt; 1.
KM RNA-directed DNA polymerase; Transferase.
FT NON TER 1
SQ SEQUENCE 873 AA; 99548 MW; F7E21804861A541 CRC64;

Query Match 65.6%; Score 42; DB 6; Length 873;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLW 9
Db 812 WKDPTNLW 820

RESULT 25
ID Q9WR73 PRELIMINARY; PRT; 874 AA.
AC Q9WR73;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pol (Fragment).
GN GAG-POL OR POL.
OS Sheep pulmonary adenomatosis virus (Jaagsiekte sheep retrovirus)
OS (JSRV).
OC Viruses; Retroid viruses; Retroviridae; Betaretrovirus.
OC NCBI_TaxID=11746;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JSRV21;
RX MEDLINE=99329222; PubMed=10400795;
RA Palmatini M., Sharp J.M., de las Heras M., Fan H.,
RT "Jaagsiekte sheep retrovirus is necessary and sufficient to induce a
RT contagious lung cancer in sheep."
RL J. Virol. 73:6964-6972(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=JSRV21;
RA Palmatini M., Sharp J.M., Fan H.,
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
CC (BY SIMILARITY).
DR EMBL: AF105220; AAD45226.1; -
DR HSP: P03355; 1MML.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0004519; F:endonuclease activity; IEA.
DR GO: GO:0016787; F:hydrolyase activity; IEA.
DR GO: GO:0008907; F:integrase activity; IEA.
DR GO: GO:0004523; F:ribonuclease H activity; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0015074; P:DNA integration; IEA.
DR GO: GO:0006310; P:DNA recombination; IEA.
DR GO: GO:0006278; P:RNA dependent DNA replication; IEA.
DR InterPro: IPR001037; Integrase_C.
DR InterPro: IPR003308; Integrase_Zn.
DR InterPro: IPR002156; RNaseH.
DR InterPro: IPR001584; Rve.
DR InterPro: IPR000477; RVTse.
DR Pfam: PF00552; Integrase_1.
DR Pfam: PF02022; Integrase_Zn_1.
DR Pfam: PF00075; RNaseH_1.
DR Pfam: PF00665; Ive; 1.
DR Pfam: PF00078; Ivt; 1.
KM Endonuclease; Hydrolyase; Nucleotidyltransferase; Polyprotein;
KM RNA-directed DNA polymerase; Transferase.
FT NON TER 1
SQ SEQUENCE 874 AA; 99701 MW; 85AC1ADE4DB97DB8 CRC64;

Query Match 65.6%; Score 42; DB 15; Length 874;

Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLW 9
Db 813 WMDPPTNLW 821

RESULT 26

Q9AYF3 PRELIMINARY; PRT; 312 AA.
AC Q9AYF3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative protein.
GN OSUNBA009409.17.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhacroidae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA See L.H., Spiegel L.A., Nascimento L.U., de la Bastide M.,
RA Preston R.R., Huang E.N., Rodriguez M.A., Vil M.D., Baker J.P.,
RA Bahret A., Shah R.S., Miller B., Kirchoff K.A., King L., Toth K.,
RA O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
RT "Genomic Sequence for Oryza sativa, Nipponbare strain, Chromosome X,
RT Clone OSUNBA009409, complete sequence."
RN Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA McCombie W.R.;
RN Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
RL [3]
RP SEQUENCE FROM N.A.
RA McCombie W.R.;
RN Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Bal H.P., See L.H., Spiegel L.A., Nascimento L.U., de la Bastide M.,
RA Preston R.R., Huang E.N., Rodriguez M.A., Vil M.D., Baker J.P.,
RA Bahret A., Shah R.S., Miller B., Kirchoff K.A., King L., Toth K.,
RA O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC078839; AK13101.1; -
DR Gramene; Q9AYF3; -
DR InterPro; IPR006652; Kelch_rep.
DR Pfam; PF01344; Kelch; 3
DR SMART; SM00612; Kelch; 3
SQ SEQUENCE 312 AA; 34374 MW; 58818D5F80AF7EBF CRC64;

Query Match 64.8%; Score 41.5; DB 10; Length 312;
Best Local Similarity 63.6%; Pred. No. 53;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 WYDPLTKLW 10
Db 97 WSYDPLCRLW 107

RESULT 27

Q7XF24 PRELIMINARY; PRT; 312 AA.
AC Q7XF24;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
GN OSUNBA009409.17.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhacroidae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
RT chromosome 10."
RN Science 300:1566-1569 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AE017089; AAP5353.1; -
KW Hypothetical protein.
SQ SEQUENCE 312 AA; 34374 MW; 58818D5F80AF7EBF CRC64;

Query Match 64.8%; Score 41.5; DB 10; Length 312;
Best Local Similarity 63.6%; Pred. No. 53;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 WYDPLTKLW 10
Db 97 WSYDPLCRLW 107

RESULT 28

Q9R728 PRELIMINARY; PRT; 144 AA.
AC Q9R728;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Z12F protein.
GN Z12F.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Z17561;
RA Fallarino A.;
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ231083; CA13125.1; -
DR InterPro; IPR000160; GGDEF.
DR Pfam; PF00990; GGDEF; 1.
DR PROSITE; PS50887; GGDEF; 1.
SQ SEQUENCE 144 AA; 17072 MW; 802739AD8A823D5A CRC64;

Query Match 64.1%; Score 41; DB 2; Length 144;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLW 8
Db 91 WHDPLTRL 98

RESULT 29

O87030 PRELIMINARY; PRT; 168 AA.
AC O87030;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Z13F protein (Fragment).
GN Z13F.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.

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OX NCBI_Taxid=666;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=217561;
RA Fallarino A.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ231085; CA13127.1; -
DR InterPro; IPR000160; GGDEF.
DR Pfam; PF00990; GGDEF.1.
DR PROSITE; PS50867; GGDEF.1.
FT NON_TER
RN [1]
SQ SEQUENCE 168 AA; 19864 MW; A2A14C6C76388FBD CRC64;

Query Match
Best Local Similarity 64.1%; Score 41; DB 2; Length 168;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKL 8
DB 115 WHDPLTRL 122

RESULT 30
Q88XC1 PRELIMINARY; PRT; 309 AA.
AC Q88XC1;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Homocysteine S-methyltransferase (EC 2.1.1.10).
LN LP_1298.
GN Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_Taxid=1590;
RN [1]
SQ SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCF51;
RC MEDLINE=22480296; PubMed=12565656;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Grooc M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Slezew R.U.;
RT "Complete genome sequence of Lactobacillus plantarum WCF51.";
RT Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935255; CAD63793.1; -
DR GO; GO:0008898; P:homocysteine S-methyltransferase activity; IEA.
DR GO; GO:0008168; P:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003726; S_methyl_trans.
DR Pfam; PF02574; S_methyl_trans.1.
DR Methyltransferase; Transferase; Complete proteome.
SQ SEQUENCE 309 AA; 32891 MW; B0C85992D25C1333 CRC64;

Query Match
Best Local Similarity 75.0%; Score 41; DB 16; Length 309;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLW 9
DB 252 YDPLTKW 259

RESULT 31
Q8VWL8 PRELIMINARY; PRT; 514 AA.
AC Q8VWL8;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Beta-mannosidase (Beta-mannosidase enzyme).
DR Lycopersicon esculentum (Tomato).

OX Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_Taxid=4081;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=cv. Glamour;
RA Mo B., Bewley J.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Glamour;
RA Mo B., Bewley J.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Glamour; TISSUE=Seed;
RA Mo B., Bewley J.;
RT "Lycopersicon esculentum beta-mannosidase (Lewside) gene encoding
RT beta-mannosidase enzyme, complete sequence.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF413204; AL37719.1; -
DR EMBL; AF403444; AL37714.1; -
DR GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001360; Glyco_hydro_1.
DR Pfam; PF00232; Glyco_hydro_1.1.
DR PRINTS; PR00131; GLYDRIASE1.
DR Prodom; PD000650; Glyco_hydro_1.1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2.1.
SQ SEQUENCE 514 AA; 59288 MW; 0A3859084EBA1971 CRC64;

Query Match
Best Local Similarity 85.7%; Score 41; DB 10; Length 514;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTK 7
DB 281 WYDPLTK 287

RESULT 32
Q81V89 PRELIMINARY; PRT; 539 AA.
AC Q81V89;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE L-lactate permease.
LN LLDLP-1 OR BA0610.
GN Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=198094;
RN [1]
SQ SEQUENCE FROM N.A.
RC MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rillestone J., Wu M.,
RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madhu R., Daugherty S.C., Durkin A.S., Hatt D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Kadane D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plant R.D., Wolf A.M., Watkins K.L., Niernan W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salberg S.L.,
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RT Nature 423:81-86(2003).
RL EMBL; AE017026; AAP24628.1; -
DR TIGR; BA0610; -
DR GO; GO:0015129; P:lactate transporter activity; IEA.
DR GO; GO:0015727; P:lactate transport; IEA.
DR InterPro; IPR003804; Lactate_perm.
DR Pfam; PF02652; Lactate_perm.1.
DR TIGRPFMS; TIGR00795; lctP.1.
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KW Complete proteome.
SQ SEQUENCE 539 AA; 57559 MW; 6D18C32DA39DCEA3 CRC64;

Query Match
Best Local Similarity 64.1%; Score 41; DB 16; Length 539;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 2 YDPLTKML 10
   ||| : ||
   8 YDPLNNIWL 16

RESULT 33
081113 PRELIMINARY; PRT; 539 AA.
ID 081113
AC 081113
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE L-lactate permease.
GN BC0612.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatchel V., Bhattacharya A., Resnik G., Mkhailova N., Lapidus A.,
RA Chu L., Mazur M., Goldsman E., Resnik N., D'Souza M., Malunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fongstein M., Ehrlich S.D.,
RA Overbeek R., Kyriides N.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL; AE016999; AAP07630.1;
DR GO; GO:0015129; P:lactate transporter activity; IEA.
DR GO; GO:0015727; P:lactate transport; IEA.
DR InterPro; IPR003804; Lactate_perm.
DR Pfam; PF02652; Lactate_perm; 1.
DR TIGRFAMs; TIGR00795; lctp; 1.
KW Complete proteome.
SQ SEQUENCE 539 AA; 57523 MW; E3891C8E9CD48ABA CRC64;

Query Match
Best Local Similarity 64.1%; Score 41; DB 16; Length 539;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 2 YDPLTKML 10
   ||| : ||
   8 YDPLNNIWL 16

RESULT 34
07VIF7 PRELIMINARY; PRT; 591 AA.
ID 07VIF7
AC 07VIF7
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE L-lactate permease (EC 2.7.1.69).
GN LUDP OR H00649.
OS Helicobacter hepaticus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=32025;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 51449 / 3B1;
RX MEDLINE=22709201; PubMed=12810954;
RA Suerbaum S., Josenhans C., Sterzenbach T., Dreescher B., Brandt P.,
RA Bell M., Droege M., Farman B., Fischer H.-P., Ge Z., Hoerster A.,
RA Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,

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RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
RT "The complete genome sequence of the carcinogenic bacterium
RT Helicobacter hepaticus."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
DR EMBL; AE017146; AAP77246.1;
KW Transferrase; Complete proteome.
SQ SEQUENCE 591 AA; 63491 MW; BCE79F374AA462DA CRC64;

Query Match
Best Local Similarity 64.1%; Score 41; DB 16; Length 591;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 2 YDPLTKML 10
   ||| : ||
   8 YDPLNNIWL 16

RESULT 35
08A125 PRELIMINARY; PRT; 604 AA.
ID 08A125
AC 08A125
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Beta-galactosidase.
GN BT3513.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076(2003).
DR EMBL; AE016940; AA078619.1;
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR006102; Glyco_hydro_21g.
DR InterPro; IPR006104; Glyco_hydro_25b.
DR InterPro; IPR04792; HI0933_like.
DR Pfam; PF00703; Glyco_hydro_2; 1.
DR Pfam; PF02837; Glyco_hydro_2_N; 1.
DR ProDom; PD018041; HI0933_like; 1.
KW Complete proteome.
SQ SEQUENCE 604 AA; 68822 MW; 75E369E21AC6834D CRC64;

Query Match
Best Local Similarity 64.1%; Score 41; DB 16; Length 604;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 1 WYDPLTKML 9
   ||| : ||
   193 WYTPVTGIW 201

RESULT 36
09K0R4 PRELIMINARY; PRT; 655 AA.
ID 09K0R4
AC 09K0R4
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE GGBP family protein.
GN VC1934.
OS Vibrrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;

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RN [1]
RC STRAIN=EI TOR N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heideberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayan L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Olin H., Dragoi I., Sellers P.,
RA McDonald L., Ueberlack T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.D., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
DR EMBL: AE004269; AAF95082.1; -
DR PIR: P82138; P82138.
DR TIGR: VCI1934; -
DR InterPro: IPR001633; EAL.
DR InterPro: IPR00160; GGDEF.
DR Pfam: PF00563; EAL; 1.
DR Pfam: PF00990; GGDEF; 1.
DR SMART: SM00267; DUF1; 1.
DR SMART: SM00552; DUF2; 1.
DR TIGRFAMs: TIGR00254; GGDEF; 1.
DR PROSITE: PS00883; EAL; 1.
DR PROSITE: PS00887; GGDEF; 1.
DR Complete proteome.
SQ SEQUENCE 655 AA; 76008 MW; 5B6F30F3904D348 CRC64;

Query Match
Best Local Similarity 64.1%; Score 41; DB 16; Length 655;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKL 8
Db 213 WYDPLTKL 220

RESULT 37
Q910K3 PRELIMINARY; PRT; 672 AA.
ID Q910K3;
AC Q910K3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein PA2635.
GN PA2635.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.D., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,
RA Gatter R.L., Goltzy L., Tolentino E., Westbrock-Madman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Mu Z., Paulsen I.T.,
RA Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL: AE004692; AAG06023.1; -
DR PIR: H83315; H83315.
DR InterPro: IPR008557; DUF839.
DR InterPro: IPR006311; Tat.
DR Pfam: PF05787; DUF839; 1.
DR TIGRFAMs: TIGR01409; Tat_signal_seq; 1.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 672 AA; 73886 MW; 364AB67B411CFC80 CRC64;

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Query Match
Best Local Similarity 64.1%; Score 41; DB 16; Length 672;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WYDPLTKL 10
Db 566 WYDPLTKL 575

RESULT 38
O8L1Z1 PRELIMINARY; PRT; 694 AA.
ID O8L1Z1;
AC O8L1Z1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Exonuclease V alpha subunit RecD.
GN RECD.
OS Pseudomonas syringae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=317;
RN [1]
RP SEQUENCE FROM N.A.
RA Regha K., Ray M.K.;
RT "recD gene is essential for growth at low temperature in the Antarctic
RT psychrotrophic bacterium Pseudomonas syringae."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY078390; AAL79573.1; -
DR GO: GO:0009338; C:exodeoxyribonuclease V complex; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0008854; F:exodeoxyribonuclease V activity; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR000585; Hemopexin.
DR InterPro: IPR006344; RecD.
DR SMART: SM00382; AAA; 1.
DR TIGRFAMs: TIGR01447; recD; 1.
DR PROSITE: PS00024; HEMOPEXIN; 1.
DR ATP-binding.
SQ SEQUENCE 694 AA; 76075 MW; FF4D48115D47B10C CRC64;

Query Match
Best Local Similarity 64.1%; Score 41; DB 2; Length 694;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKL 10
Db 375 WYDPLTKL 384

RESULT 39
Q7UTU4 PRELIMINARY; PRT; 733 AA.
ID Q7UTU4;
AC Q7UTU4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN RBL105.
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Planctomycetales.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Planctomycete
RT strain 1."

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RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
 DR EMBL; BX294152; CAD77137.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 733 AA; 81016 MW; 4432EA709BBF62E CRC64;

Query Match 64.1%; Score 41; DB 16; Length 733;
 Best Local Similarity 70.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WDPLTKLWL 10
 DB 451 WDPNGKLWL 460

RESULT 40

070021 PRELIMINARY; PRT; 808 AA.
 AC 070021;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Beta-glucosidase.
 GN ERYBI.
 OS Saccharopolyspora erythraea (Streptomyces erythraeus).
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Pseudonocardiales; Pseudonocardaceae; Saccharopolyspora.
 OK NCBI_TaxId=1836;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL2338;
 RX MEDLINE=98273631; PubMed=9613575;
 RA Galsner S., Boehm G.A., Douthett M., Raynal M.C., Dillon N.,
 RA Cortes J., Leadley P.F.,
 RT "Analysis of Eryd and ErydII from the erythromycin biosynthetic gene
 RT cluster in Saccharopolyspora erythraea.";
 RL Mol. Gen. Genet. 258:78-88 (1998).
 DR EMBL; Y14327; CAA74702.1; -
 DR GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR002772; Glyco_hydro_3C.
 DR InterPro; IPR001764; Glyco_hydro_3N.
 DR Pfam; PF00933; Glyco_hydro_3; 1.
 DR Pfam; PF01915; Glyco_hydro_3_C; 1.
 DR PRINTS; PR00133; GMDRLASE3.
 SQ SEQUENCE 808 AA; 86677 MW; 0C619016CC00A751 CRC64;

Query Match 64.1%; Score 41; DB 2; Length 808;
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 DPLTKLWL 10
 DB 61 DPLAKLWL 68

RESULT 41

07Y308 PRELIMINARY; PRT; 111 AA.
 ID 07Y308;
 AC 07Y308;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN RB49ORF095C.
 OS Enterobacteria phage RB49.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC T4-like viruses.
 OK NCBI_TaxId=50948;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97250366; PubMed=9096222;
 RA Monod C., Repolia F., Kutateladze M., Tatar F., Kirsch H.M.;
 RT "The genome of the pseudo T-even bacteriophages, a diverse group that

RT resembles T4.";
 RL J. Mol. Biol. 267:237-249 (1997).

[2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21062343; PubMed=11092834;
 RA Ang D., Keppel F., Klein G., Richardson A., Georgopoulos C.;
 RT "Genetic analysis of bacteriophage-encoded coxapoxonins.";
 RL Annu. Rev. Genet. 34:439-456 (2000).

[3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21972795; PubMed=11976309;
 RA Desplats C., Dez C., Tatar F., Eleaume H., Kirsch H.M.;
 RT "Snapshot of the genome of the pseudo-T-even bacteriophage RB49.";
 RL J. Bacteriol. 184:2789-2804 (2002).

[4]
 RP SEQUENCE FROM N.A.
 RA Tatar F., Desplats C., Kutateladze M., Monod C., Ackermann H.-W.,
 RA Kirsch H.M.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

[5]
 RP SEQUENCE FROM N.A.
 RA Kirsch H.M.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

[6]
 RP SEQUENCE FROM N.A.
 RA Ang D., Richardson A., Mayer M.P., Keppel F., Kirsch H.,
 RA Georgopoulos C.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

[7]
 RP SEQUENCE FROM N.A.
 RA Zhao L., Tatar F., Kirsch H.M., Aisaka F.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

[8]
 RP SEQUENCE FROM N.A.
 RA Desplats C., Dez C., Tatar F., Eleaume H., Kirsch H.M.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

[9]
 RP SEQUENCE FROM N.A.
 RA Thiemer C.A., Desplats C., Dez C., Tatar F., Eleaume H., Kirsch H.M.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

[10]
 RP SEQUENCE FROM N.A.
 RA Desplats C., Dez C., Tatar F., Eleaume H., Kirsch H.M.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

[11]
 RP SEQUENCE FROM N.A.
 RA Kirsch H.M.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

[12]
 RP SEQUENCE FROM N.A.
 RA Desplats C., Kirsch H.M.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

[13]
 RP SEQUENCE FROM N.A.
 RA Letarov A.V., Kirsch H.M., Tatar F.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

[14]
 RP SEQUENCE FROM N.A.
 RA Bertrand C., Petrov V., Nolan J., Letarov A., Desplats C., Chin D.,
 RA Karam J.D., Kirsch H.M.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY343333; AA015351.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 111 AA; 13073 MW; 94EB50A5E9E5023D CRC64;

Query Match 62.5%; Score 40; DB 9; Length 111;
 Best Local Similarity 85.7%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DPLTKLWL 9
 DB 39 DPLTKLWL 45

RESULT 42

087XC5 PRELIMINARY; PRT; 173 AA.
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE NAD (P)H dehydrogenase, quinone family.
 GN PEPY04258.
 OS Pseudomonas syringae (pv. tomato).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=323;
 RN [1]

SEQUENCE FROM N.A.

RC STRAIN=DC3000;
 RA Beil R., Uardar V., Khouri H., Fedorova N., Tran B., Russell D.,
 RA Berry K., Uterback T., Van Aken S., Feldblum T., Gwin M.,
 RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
 RA Brinkac L., Beaman M., Haft D., Selengut J., Nelson W., Davidsen T.,
 RA White O., Fraser C., Collier A., "Complete sequence of Pseudomonas syringae."
 RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RI EMBL; AB016871; AA05712.1; -.
 DR TIGR; PEPY04258; -.
 DR GO; GO:0003955; P:NAD(P)H dehydrogenase (quinone) activity; IEA.
 DR CO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR003680; NADrdh.2.
 DR Pfam; PF02525; Flavodoxin_2; 1.
 KM Complete proteome.
 SQ SEQUENCE 173 AA; 19828 MW; F717A393A8607E4B CRC64;

Query Match 62.5%; Score 40; DB 16; Length 173;
 Best Local Similarity 58.3%; Pred. No. 53;
 Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 WYD--PLTKML 10
 Db 67 WYNYPLTKML 78

RESULT 43

0817A3 PRELIMINARY; PRT; 230 AA.

AC 0817A3;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Paired box protein (fragment).
 GN PAX258.
 OS Platyneris dumerilii (dumeril's clam worm).
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;
 OC Phyllococida; Nereididae; Platyneris.
 OX NCBI_TaxID=6359;
 RN [1]

SEQUENCE FROM N.A.

RA Zelada F., Burgdorf C., Steimetz P., de Campos-Baptista M.I.M.,
 RA Witbrodt J., Arend D.,
 RT "The transition from radial to bilateral symmetry in bilaterian
 ontogeny and evolution."
 RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AJ505023; CAD3608.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR001523; Paired_box.
 DR Pfam; PF00292; PAX; 1.
 DR PRINTS; PR00027; PAIRDBOX.
 DR SMART; SM00351; PAX; 1.
 DR PROSITE; PS00034; PAIRED_BOX; 1.
 FT NON_TER 1
 FT 230

SEQUENCE 230 AA; 24965 MW; D08E417AF3546F17 CRC64;

Query Match 62.5%; Score 40; DB 5; Length 230;
 Best Local Similarity 75.0%; Pred. No. 71;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKL 8
 Db 210 WFDPLYTKL 217

RESULT 44

08WST5 PRELIMINARY; PRT; 305 AA.

AC 08WST5;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Gamone 1

BLEPHARMONE.

OS Blepharisma japonicum.
 OC Eukaryota; Alveolata; Ciliophora; Heterotricha; Heterotrichida;
 OC Blepharismidae; Blepharisma.
 OX NCBI_TaxID=5961;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21592973; PubMed=11724922;
 RA Sugita M., Harumoto T.,
 RT "Identification, characterization, and complete amino acid sequence of
 the conjugation-inducing glycoprotein (blepharmone) in the ciliate
 RT Blepharisma japonicum.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:14446-14451(2001).
 DR EMBL; AB056696; BAB78725.1; -.
 SQ SEQUENCE 305 AA; 34353 MW; 1DA6C7EA4B8FAB3 CRC64;

Query Match 62.5%; Score 40; DB 5; Length 305;
 Best Local Similarity 60.0%; Pred. No. 94;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKML 10
 Db 254 WKDPNNKMWL 263

RESULT 45

099180 PRELIMINARY; PRT; 345 AA.

AC 099180;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Terminal inverted repeats, and ORF 1.

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]

SEQUENCE FROM N.A.

RC STRAIN=Dublin;
 RX MEDLINE=91209947; PubMed=1840573;
 RA Krause M., Harwood J., Flier J., Guiney D.,
 RT "Genetic analysis of the homology between the virulence plasmids of
 RT Salmonella dublin and Yersinia pseudotuberculosis.";
 RL Infect. Immun. 59:1860-1863(1991).
 DR EMBL; M58505; AAA27173.1; -.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR InterPro; IPR001584; Rve.
 DR Pfam; PF00665; rve; 1.

SEQUENCE 345 AA; 40120 MW; EFC1298AD32387C0 CRC64;

Query Match 62.5%; Score 40; DB 2; Length 345;
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy U., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kravitski M.I., Skalska U., Smallus D.E., Schermer A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC055989, AAH55989.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 500 AA; 54722 MW; 10F16756CAFDC0B CRC64;
 Query Match 62.5%; Score 40; DB 13; Length 500;
 Best Local Similarity 55.6%; Pred. NO. 1.5e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WYDPLTKLM 9
 Db 248 WYDPLTEBW 256
 RESULT 49
 Q9VBN4 PRELIMINARY; PRT; 513 AA.
 ID 09VBN4; Q9VBN4; (TrEMBLrel. 13, Created)
 DT 01-MAR-2000 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 25, Last annotation update)
 DC C615097 protein (GH18278p).
 GN C615097.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borovaya D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.D., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ijzerman C.,
 RA Jajala M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murzy D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle D.J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skipski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svaitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein D.A., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RT Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ceiniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Barzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Drenek D., Farfan D.,
 RA Ferrizera S., Frise E., Galie R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ijzerman C., Jajala M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacle D.J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svaitskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of Drosophila melanogaster genome."
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Timp J.L., Bergman C., Bernan B., Carlson J.W., Ceiniker S.E.,
 RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smucnik F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of Drosophila melanogaster genome."
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Ceiniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacle D.J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Ceiniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB003798; AAF57630.2; -
 DR HSSP: 005516; 1CS3
 DR FLYBASE: FBgn0034396; CG15097.
 DR GO: GO:0005515; F:protein binding; IEA.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR006651; Kelch.
 DR InterPro: IPR006652; Kelch_rep.
 DR Pfam: PF00651; BTB; 1.
 DR Pfam: PF01344; Kelch; 6.
 DR PRINTS: PR00501; KXICRREPAT.
 DR PROSITE: PS0097; BTB; 1.
 SQ SEQUENCE 513 AA; 57551 MW; 20B9D4F732514834 CRC64;
 Query Match 62.5%; Score 40; DB 5; Length 513;
 Best Local Similarity 75.0%; Pred. NO. 1.6e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YDPLTKM 9
 Db 332 YDPLTKM 339

RESULT 50

Q9A9X4 PRELIMINARY; PRT; 519 AA.
 AC Q9A9X4;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Hypothetical protein CC0837.
 GN CC0837.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
 OC Caulobacteraceae; Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RC MEDLINE=21173698; PubMed=11259647;
 RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohra N., Maddock J.R.,
 RA Pococka I., Nelson W.C., Newton A., Stephens C., Madde N.D., Ely B.,
 RA Deboy R.T., Dodson R.C., Durkin A.S., Gwin M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Utecherback T., Tran K., Wolf A., Vamathavan J., Emolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL; AE005760; AK22822.1; -.
 DR PIR; B87353; B87353.
 DR TIGR; CC0837; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 519 AA; 53934 MW; F37A3A52753DB53B CRC64;

Query Match 62.5%; Score 40; DB 16; Length 519;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKM 9
 Db 414 WYAPLAGLM 422

RESULT 51

Q8NSC3 PRELIMINARY; PRT; 582 AA.
 AC Q8NSC3;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Similar to intracellular A particle-promoted polypeptide.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=uterus;
 RA Strauberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR GO; GO:0005515; F:protein binding; ISA.
 DR InterPro; IPR000210; BTR POZ.
 DR InterPro; IPR006551; Keich.
 DR InterPro; IPR006552; Keich_rep.
 DR Pfam; PF01344; Keich_1.
 DR Pfam; PF01344; Keich_6.
 DR PRINTS; PR00501; KKLCHREPEAT.

DR SMART; SM00225; BTR; 1.
 DR SMART; SM00612; Keich; 5.
 DR PROSITE; PS50097; BTR; 1.
 SQ SEQUENCE 582 AA; 65620 MW; 0233689DB32E40BD CRC64;

Query Match 62.5%; Score 40; DB 4; Length 582;
 Best Local Similarity 75.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YDPLTKM 9
 Db 363 YDPLTKM 370

RESULT 52

Q8SB55 PRELIMINARY; PRT; 612 AA.
 AC Q8SB55;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN OSUNB0091009.4.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriatoidae; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
 RA Sakai C., Henry D., Oates R., Simmons J.;
 RT "Rice Genomic Sequence."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC091732; AL77153.1; -.
 DR Gramene; Q8SB55; -.
 DR InterPro; IPR006928; Glyco_trans_6hp.
 KW Hypothetical protein.
 SQ SEQUENCE 612 AA; 68316 MW; 077322720C99E444 CRC64;

Query Match 62.5%; Score 40; DB 10; Length 612;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 WYD--PLTKML 10
 Db 419 WYDGMPLRFL 430

RESULT 53

Q7XF65 PRELIMINARY; PRT; 612 AA.
 AC Q7XF65;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN OSUNB0091009.4.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriatoidae; Oryzae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA The Rice Chromosome 10 Sequencing Consortium;
 RT "In-depth view of structure, activity, and evolution of rice
 chromosome 10."
 RL Science 300:1566-1569(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;

RA Buell C.R., Wang R.A., McCombie W.R., Messing J., Yuan Q.,
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017087; AAP5491.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 612 AA; 68316 MW; 077322720C99E444 CRC64;
 Query Match 62.5%; Score 40; DB 10; Length 612;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
 QY 1 WYD-PLTKML 10
 Db 419 WYDGMPLRLFWL 430
 RESULT 54
 Q86BFL PRELIMINARY; PRT; 617 AA.
 AC Q86BFL;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CG15097-PB.
 GN CG15097
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_Taxid=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe O., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
 RA Abril J.F., Agbayani A., An H.U., Andrews-Pfankuch C., Baldwin D.,
 RA Ballwe R.M., Basu P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison U.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Krat C., Kravitz S., Kulp D., Lai Z.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mout R.M., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacled J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard U., Puri V., Reese M.G.,
 RA Reinert C., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodcock G.M., Woodstock G.M., Yang S., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195 (2000).
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,

RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C.W., Berman B.P., Carlson J.W., Celniker S.E.,
 RA Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
 RA Harris N.L., Krommiller B., Marshall B., Millburn G.H., Richter J.,
 RA Russo S., Seale S.M.J., Smith E., Shu S., Smutnick F.,
 RA Whitefield E.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.,
 RA Lewis S.E.;
 RT "Annotation of Drosophila melanogaster genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RP [4]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB003798; AAC1354.1; -.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR InterPro; IPR000210; BTB POZ.
 DR InterPro; IPR006651; Kelch.
 DR InterPro; IPR006652; Kelch_rep.
 DR Pfam; PF00651; BTB_1.
 DR Pfam; PF01344; Kelch; 6.
 DR PRINTS; PR00501; KELCHREPEAT.
 DR SMART; SM00225; BTB; 1.
 DR SMART; SM00612; Kelch; 6.
 DR PROSITE; PSS0097; BTB; 1.
 SQ SEQUENCE 617 AA; 68742 MW; 6005927B1B9DAE2C CRC64;
 Query Match 62.5%; Score 40; DB 5; Length 617;
 Best Local Similarity 75.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 YDPLTKLM 9
 Db 436 YDPLTKLM 443
 RESULT 55
 Q8IH99 PRELIMINARY; PRT; 620 AA.
 ID Q8IH99
 AC Q8IH99;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE AT2465P (Fragment).
 GN CG15097
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_Taxid=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Change M., Chavez C., Dorsett V., Dresnek D., Fatfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo U., Pacled J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BT001347; AAN71102.1; -.
 DR FlyBase; FBgn0034396; CG15097.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR InterPro; IPR000210; BTB POZ.
 DR InterPro; IPR006651; Kelch.
 DR InterPro; IPR006652; Kelch_rep.
 DR Pfam; PF00651; BTB; 1.
 DR Pfam; PF01344; Kelch; 6.
 DR PRINTS; PR00501; KELCHREPEAT.
 DR SMART; SM00225; BTB; 1.
 DR SMART; SM00612; Kelch; 6.

DR PROSITE; P550097; BTB; 1.
 FT NON TER 1
 SQ SEQUENCE 620 AA; 69069 MW; 47CAD3F3B3A57871 CRC64;

Query Match
 Best Local Similarity 62.5%; Score 40; DB 5; Length 620;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 YDPLTKLM 9
 DB 439 YDPLTKLM 446

RESULT 56

ID Q7ZV08 PRELIMINARY; PRT; 640 AA.
 AC Q7ZV08;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Similar to NSI-binding protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxId=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Body;
 RA Struhsberg R.;
 RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC045449; AA045449.1; -
 DR GO; GO:0005515; F:protein binding; IEA.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR006651; Kelch.
 DR InterPro; IPR006652; Kelch_rep.
 DR Pfam; PF00651; BTB; 1.
 DR Pfam; PF01344; Kelch; 6.
 DR PRINTS; PRO0501; KELCHREPEAT.
 DR SMART; SM00225; BTB; 1.
 DR SMART; SM00612; Kelch; 6.
 DR PROSITE; P550097; BTB; 1.
 SQ SEQUENCE 640 AA; 71117 MW; DCCGFC2438A1D81 CRC64;

Query Match
 Best Local Similarity 62.5%; Score 40; DB 13; Length 640;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 YDPLTKLM 9
 DB 482 YDPLTKLM 489

RESULT 57

ID Q8J2J6 PRELIMINARY; PRT; 648 AA.
 AC Q8J2J6;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Putative aminoacid permease protein.
 GN AP.
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxId=5476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Prignieu O., Porta A., Maresca B.;
 RL "Identification and cloning of the CAP gene of Candida albicans";
 DR EMBL; AF441396; AA062330.1; -
 DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
 DR GO; GO:0006865; P:amino acid transport; IEA.

DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR002293; AA/rel_permease.
 DR InterPro; IPR004840; AAC_permease.
 DR InterPro; IPR004841; Permease_region.
 DR Pfam; PF00324; aa_permeases; 1.
 DR PROSITE; P500218; AMINO ACID PERMEASE 1; 1.
 SQ SEQUENCE 648 AA; 71837 MW; ACD2A16EAD5A2B CRC64;

Query Match
 Best Local Similarity 66.7%; Score 40; DB 3; Length 648;
 Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

OY 1 WY--DPLTKLM 10
 DB 593 WYLNVPPLTKFWL 604

RESULT 58

ID Q8LM21 PRELIMINARY; PRT; 713 AA.
 AC Q8LM21;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN OSUNAA0019N10.24.
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eubharoidae; Oryzae; Oryza.
 OX NCBI_TaxId=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA McCombie W.R., de la Bastide M., Spiegel L., Preston R., Ferraro K.,
 RA Kuit K., Nascimento L., Zutavern T., Balija V., Bell M., Baker J.,
 RA Miller B., Katzenberger F., Muller S., King N., Sullivan P., Yang C.,
 RA Dike S., O'Shaughnessy A., Palmer L., Dedha N.;
 RT "Genomic sequence for Oryza sativa, Nipponbare strain, clone
 RT OSUNAA0019N10, from chromosome 10, complete sequence."
 RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AC124213; AAM74466.1; -
 DR Gramene; Q8LM21; -
 DR InterPro; IPR00928; Glyco_trans_6hp.
 KM Hypothetical protein.
 SQ SEQUENCE 713 AA; 79349 MW; C170A7A096174AFB CRC64;

Query Match
 Best Local Similarity 62.5%; Score 40; DB 10; Length 713;
 Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

OY 1 WY--DPLTKLM 10
 DB 520 WYDGMPLTKFWL 531

RESULT 59

ID Q8IKY0 PRELIMINARY; PRT; 715 AA.
 AC Q8IKY0;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN PF14.0471.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxId=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3D7;

RX MEDLINE=2255705; PubMed=1236864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angiuoli S.,
RA Partea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings I.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.,
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum".
RL Nature 419:498-511(2002).
DR EMBL; AE014824; AAN37084.1; -.
KM Hypothetical protein.
SQ SEQUENCE 715 AA; 84432 MW; 0B80A721D5C3D3B6 CRC64;

QY Query Match 62.5%; Score 40; DB 5; Length 715;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Db 1 WYDPLTKLWL 10
53 WYNARTKQWL 62

RESULT 60
Q8IK14 PRELIMINARY; PRT; 979 AA.
AC Q8IK14;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical protein.
DE PF10.0026.
GN Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=2255705; PubMed=1236864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angiuoli S.,
RA Partea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings I.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.,
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum".
RL Nature 419:498-511(2002).
DR EMBL; AE014829; AAN35224.1; -.
KM Hypothetical protein.
SQ SEQUENCE 979 AA; 118671 MW; 273A0810988F5C8F CRC64;

QY Query Match 62.5%; Score 40; DB 5; Length 979;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Db 1 WYDPLTKLWL 10
957 WLDALTRQWM 966

RESULT 61
Q87YF0 PRELIMINARY; PRT; 283 AA.
AC Q87YF0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
DE PSPPO3850.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Buell R., Joaridar V., Khouri H., Fedorova N., Tran B., Russell D.,
RA Berry K., Utechtack T., Van Aken S., Feldblyum T., Gwin M.,
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA Brinkac L., Beaman M., Haft D., Selengut J., Nelson W., Davidson T.,
RA White O., Fraser C., Collier A.,
RT "Complete sequence of Pseudomonas syringae".
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016869; AA057317.1; -.
DR TIGR; PSPPO3850; -.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 283 AA; 32710 MW; E6BD39BB099277C4 CRC64;

QY Query Match 61.7%; Score 39.5; DB 16; Length 283;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
Db 1 WYDPLTKLWL 10
104 YDPRITRLWL 114

RESULT 62
Q91UW3 PRELIMINARY; PRT; 109 AA.
ID Q91UW3
AC Q91UW3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Isolate hc94 E2 (Genome polypeptide) (fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=hc94;
RA Fan X., Di Bisceglie A.M.,
RT "Genetic Characteristics of Putative Hypervariable Region (HVR1) in
RT Genotype 2 Hepatitis C virus".
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF218876; AAF80573.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR002531; HCV NS1.
DR Pfam; PF01539; HCV env; I.
DR Pfam; PF01560; HCV NS1; I.
DR ProDom; PD186062; HCV NS1; I.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polypeptide; Transmembrane.
FT NON TER 1
SQ SEQUENCE 109 AA; 12115 MW; B04123BF1E056C7A CRC64;

QY Query Match 60.9%; Score 39; DB 12; Length 109;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db 1 WYDPLTKLWL 10
92 YIQPIQLWL 101

RESULT 63

Q54791 PRELIMINARY; PRT; 155 AA.
 AC Q54791;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE TSP0 protein.
 GN TSP0.
 OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 OC Rhodobacteraceae; Rhodobacter.
 OX NCBI_TaxID=1063;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lang H.P.;
 RT "Rhodobacter sphaeroides carotenoid genes."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ010302; CAB38741.1; -.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR InterPro: IPR004307; TSP0_MBR.
 DR Pfam: PF03073; TSP0_MBR; 1.
 DR Prodom: PD006774; TSP0_MBR; 1.
 SQ SEQUENCE 155 AA; 17609 MW; 75A728BBA9CF2C5B CRC64;

Query Match 60.9%; Score 39; DB 2; Length 155;
 Best Local Similarity 66.7%; Pred. No. 71;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
 |||
 DB 28 WYDNINKPW 36

RESULT 64

Q9RFC8 PRELIMINARY; PRT; 158 AA.
 AC Q9RFC8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE TSP0.
 OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 OC Rhodobacteraceae; Rhodobacter.
 OX NCBI_TaxID=1063;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2.4.1;
 RA Choudhary M., Kaplan S.;
 RT "DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2.4.1."
 RL Nucleic Acids Res. 0:0-0(2000).
 DR EMBL: AF195122; AAF24291.1; -.
 DR PIR: A57438; A57438.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR InterPro: IPR004307; TSP0_MBR.
 DR Pfam: PF03073; TSP0_MBR; 1.
 DR Prodom: PD006774; TSP0_MBR; 1.
 SQ SEQUENCE 158 AA; 17976 MW; 16569B7156AFD0CD CRC64;

Query Match 60.9%; Score 39; DB 2; Length 158;
 Best Local Similarity 66.7%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
 |||
 DB 30 WYDNINKPW 38

RESULT 65

Q848N8

ID Q848N8 PRELIMINARY; PRT; 176 AA.

AC Q848N8;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE YabF.
 GN YABF.
 OS Gamma-proteobacterium Hec 75m4.
 OC Plasmid pAK116.
 OC Bacteria; environmental samples.
 OX NCBI_TaxID=77133;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22507661; PubMed=12620823;
 RA Knietech A., Maechkowitz T., Bowlen S., Henne A., Daniel R.;
 RT "Construction and Screening of Metagenomic Libraries Derived from Enrichment Cultures: Generation of a Gene Bank for Genes Confering Alcohol Oxidoreductase Activity on Escherichia coli.";
 RL Appl. Environ. Microbiol. 69:1408-1416(2003).
 DR EMBL: AF543470; AAO59932.1; -.
 DR GO: GO:0046821; C:extrachromosomal DNA; IEA.
 DR GO: GO:0003955; F:NAD(P)H dehydrogenase (quinone) activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR003680; NADPHdh_2.
 DR Pfam: PF02525; Flavodoxin_2; 1.
 KW Plasmid.
 SQ SEQUENCE 176 AA; 20179 MW; ED92C4B3C89FCCA5 CRC64;

Query Match 60.9%; Score 39; DB 2; Length 176;
 Best Local Similarity 58.3%; Pred. No. 80;
 Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD--PLTKML 10
 |||
 DB 67 WYSTPPLTKLMM 78

RESULT 66

Q9GLF8 PRELIMINARY; PRT; 177 AA.
 AC Q9GLF8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Pol protein (Fragment).
 GN Pol.
 OS Trichosurus vulpecula (Brush-tailed possum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
 OX NCBI_TaxID=9337;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21105294; PubMed=11160757;
 RA Baillie G.J., Wilkins R.J.;
 RT "Endogenous Type D Retrovirus in a Marsupial, the Common Brush-tail possum (Trichosurus vulpecula)."
 RL J. Virol. 75:2499-2507(2001).
 DR EMBL: AF284693; AAG28160.1; -.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR GO: GO:0008907; F:integrase activity; IEA.
 DR GO: GO:0006310; P:DNA recombination; IEA.
 DR InterPro: IPR001037; Integrase_C.
 DR InterPro: IPR001584; Rve.
 DR Pfam: PF00552; Integrase; 1.
 DR Pfam: PF00665; Rve; 1.
 FT NON TER
 SQ SEQUENCE 177 AA; 20044 MW; AB51BDP92573E2F6 CRC64;

Query Match 60.9%; Score 39; DB 6; Length 177;
 Best Local Similarity 66.7%; Pred. No. 81;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9

Db 127 WKDPLTHQW 135

RESULT 67

Q9CPE6 PRELIMINARY; PRT; 240 AA.
 ID Q9CPE6
 AC Q9CPE6
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE HOPD.
 GN HOPD OR PM0087.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Pm70;
 RX MEDLINE=21145866; PubMed=11248100;
 RT May B.J., Zhang Q., Li L.L., Paustian M.L., Whitam T.S., Kapur V.,
 "Complete genomic sequence of Pasteurella multocida Pm70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).
 DR EMBL; AE006044; AAK02171.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000045; Peptidase_A24a.
 DR Pfam; PF01478; Peptidase_A24; 1.
 KW Complete proteome.
 SQ SEQUENCE 240 AA; 27795 MW; 3FC8C0F8ED8DC9F6 CRC64;

Query Match 60.9%; Score 39; DB 16; Length 240;
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

Qy 1 WYDP-LTKLWL 10
 Db 229 WYSPSWSKLM 240

RESULT 68
 Q96YU1 PRELIMINARY; PRT; 274 AA.
 ID Q96YU1
 AC Q96YU1
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein ST2085.
 GN ST2085.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=11955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX MEDLINE=21456156; PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 Sekine M., Baba S.-I., Anai A., Kosugi H., Hosoyama A., Fukui S.,
 Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
 Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 Oshima T., Kikuchi H.,
 "Complete genome sequence of an aerobic thermacidophilic
 Crenarchaeon, Sulfolobus tokodaii strain17.";
 RT DNA Res. 8:133-140 (2001).
 DR EMBL; AP000988; BAB67185.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR000620; DUF6.
 DR Pfam; PF00892; DUF6; 2.
 KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 274 AA; 30296 MW; AB4707081FDD2A27 CRC64;

Query Match 60.9%; Score 39; DB 17; Length 274;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WYDPLTKL 8
 Db 215 WYDALTKL 222

RESULT 69

Q9LYY7 PRELIMINARY; PRT; 335 AA.
 ID Q9LYY7
 AC Q9LYY7
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN F15A17.10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Terry N., Ardiles W., Buyschaert C., Dasseville R.,
 De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
 Villarroel R., Gielen J., Van Montagu M., Bantrott I., Mewes H.W.,
 Rudd S., Lemcke K., Mayer K.F.X.;
 Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL163002; CAB86065.1; -;
 DR PIR; T48319; T48319.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR006652; Kelch_rep.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF01344; Kelch; 2.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00612; Kelch; 1.
 DR PROSITE; PS50181; FBOX; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 335 AA; 38512 MW; CFSBD29DB01DDC26 CRC64;

Query Match 60.9%; Score 39; DB 10; Length 335;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLWL 10
 Db 176 YDPTQTWL 184

RESULT 70

Q9T035 PRELIMINARY; PRT; 365 AA.
 ID Q9T035
 AC Q9T035
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN T22F8.190 OR AT4G39290.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Bevan M., Zimmermann W., Grueneisen A., Wambutt R., Bancroft I.,
 RA Mewes H.W., Mayer K.F.X., Scheller C.;
 RA Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
 RA Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AL050351; CAB3644.1; -
 DR EMBL; AL161595; CAB80592.1; -
 DR PIR; T08577; T08577.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR00652; Kelch_rep.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF01344; Kelch; 2.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00612; Kelch; 2.
 KM Hypothetical protein.
 SQ SEQUENCE 365 AA; 42172 MW; F7187A0F9686E01B CRC64;
 Query Match 60.9%; Score 39; DB 10; Length 365;
 Best Local Similarity 55.6%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 WYDPTKLM 9
 Db 272 WYDSCRKIM 280
 RESULT 71
 AC Q9W3D5 PRELIMINARY; PRT; 403 AA.
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE CG12081 protein (LD20420P).
 GN CG12081.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCB1_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; Pubmed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe C.M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Baas A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.A., Bouck J., Brockstein P., Brothier P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes W., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrelira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveli J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Paclob J., Paragosa V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celinker S.;
 RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AE003444; AAF46395.1; -
 DR EMBL; AY119599; AAM50253.1; -
 DR Flybase; FBgn030053; CG12081.
 DR InterPro; IPR00652; Kelch_rep.
 DR Pfam; PF01344; Kelch; 5.
 SQ SEQUENCE 403 AA; 45202 MW; BEC052258CF3DB95 CRC64;
 Query Match 60.9%; Score 39; DB 5; Length 403;
 Best Local Similarity 75.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 YDPTKLM 9
 Db 272 FDPRTKLM 279
 RESULT 72
 AC O17702 PRELIMINARY; PRT; 430 AA.
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE C53A5.11 protein.
 GN C53A5.11.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OC NCB1_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mortimore B.J.;
 RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99069613; Pubmed=9851916;
 RX none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL; Z81486; CAB03991.1; -
 DR PIR; T20170; T20170.
 DR WormPep; C53A5.11; CE08960.

DR GO:0004289; F:subtilase activity; IEA.
 DR GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR006652; Kelch rep.
 DR InterPro: IPR00209; Peptidase_S8.
 DR Pfam: PF01344; Kelch; 5.
 DR SMART: SM00612; Kelch; 4.
 DR PROSITE: PS00136; SUBTILASE ASP; 1.
 SQ SEQUENCE 430 AA; 48768 MW; 46576ARCAD2B8420 CRC64;

Query Match
 Best Local Similarity 60.9%; Score 39; DB 5; Length 430;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9
 DB 372 YDPLTKLM 379

RESULT 73
 ID Q7UA40 PRELIMINARY; PRT; 440 AA.
 AC Q7UA40;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative glycosyltransferase.
 GN SYN0060.
 OS Synecchococcus sp. (strain WH6102).
 OC Bacteria; Cyanobacteria; Chroococcales; Synecchococcus.
 OX NCBI_TaxID=84588;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=2825697; PubMed=12917641;
 RA Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P.,
 RA Lamerdin J., Regala W., Allen E.E., McCarron J., Paulsen I.,
 RA Duxreane A., Partensky F., Webb E.A., Waterbury J.;
 RT "The genome of a motile marine Synecchococcus.";
 RL Nature 424:1037-1042(2003).
 DR EMBL: BX569689; CA06575.1; -
 KW Transference; Complete proteome.
 SQ SEQUENCE 440 AA; 48530 MW; CA8B56C637E674FA CRC64;

Query Match
 Best Local Similarity 60.9%; Score 39; DB 16; Length 440;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKM 9
 DB 31 WYDPMKSLM 39

RESULT 74
 ID 017700 PRELIMINARY; PRT; 480 AA.
 AC 017700;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C53A5.9 protein.
 GN C53A5.9.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peleiderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mortimore B.J.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for

RT Investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL: Z81486; CAB03989.1; -
 DR PIR: T20168; T20168.
 DR WormPep: C53A5.9; CE08958.
 DR GO:0005634; C:nucleus; IEA.
 DR GO:0000074; P:regulation of cell cycle; IEA.
 DR InterPro: IPR004367; Cyclin_Cterm.
 DR InterPro: IPR006651; Kelch.
 DR InterPro: IPR006652; Kelch rep.
 DR Pfam: PF02984; cyclin_C_1.
 DR Pfam: PF01344; Kelch; 5.
 DR PRINTS: PR00501; KELCHREPEAT.
 DR SMART: SM00612; Kelch; 4.
 SQ SEQUENCE 480 AA; 5409 MW; 15BD00360DB5A199 CRC64;

Query Match
 Best Local Similarity 60.9%; Score 39; DB 5; Length 480;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9
 DB 396 YDPLTKLM 403

RESULT 75
 ID Q88G73 PRELIMINARY; PRT; 518 AA.
 AC Q88G73;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN PP3852.
 OS Pseudomonas putida (strain KT2440).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=160488;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22423060; PubMed=12534463;
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
 RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
 RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
 RA Chris Lee P., Holtzapfle E., Scanlan D., Tran K., Moazzes A.,
 RA Uteback T., Rizzo M., Lee K., Kosack D., Moestl D., Medler H.,
 RA Lauber J., Stjepandic D., Hoheisel J., Streitz M., Heim S.,
 RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tnemler B.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative analysis of the
 RT metabolically versatile Pseudomonas putida KT2440.";
 RL Environ. Microbiol. 4:799-808(2002).
 DR EMBL: AB016788; AAN69446.1; -
 DR TIGR: PP3852; -

DR GO:0005622; C:intracellular; IEA.
 DR GO:0005840; C:ribosome; IEA.
 DR GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro: IPR000595; GMP_binding.
 DR InterPro: IPR008195; Ribosomal_L34E.
 DR PROSITE: PS00888; GMP_BINDING_1; 1.
 DR PROSITE: PS01145; RIBOSOMAL_L34E; 1.
 DR KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 518 AA; 57793 MW; 9314E04F3CC9DB6D CRC64;

Query Match
 Best Local Similarity 60.9%; Score 39; DB 16; Length 518;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 10
 DB 244 WYDPMKSLM 253


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RESULT 76
ID 024953 PRELIMINARY; PRT; 551 AA.
AC 024953;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE L-lactate permease (LCTP).
GN Hpo141.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kervatage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khaila S.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
DR EMBL; AE000535; AAD07209.1; -.
DR PIR; E64537; E64537.
DR TIG; Hpo141; -.
DR GO; GO:0015129; F:lactate transporter activity; IEA.
DR GO; GO:0015727; P:lactate transport; IEA.
DR InterPro; IPR003804; Lactate perm.
DR Pfam; PF02652; Lactate_perm; 1.
DR TIGRFAMs; TIGR00795; lctp; 1.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 551 AA; 59407 MW; 3776DA2E7824C7C CRC64;

Query Match 60.9%; Score 39; DB 16; Length 551;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLWL 10
Db 8 YDPLGNLWL 16

RESULT 77
ID 09ZMT9 PRELIMINARY; PRT; 551 AA.
AC 09ZMT9;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE L-lactate permease.
GN LUDP 2 OR JHP0129.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C.,
RA Smith D.R., Noonan B., Guild B.C., deLonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
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RT Gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
DR EMBL; AE001452; AAD05719.1; -.
DR PIR; D71969; D71969.
DR GO; GO:0015129; F:lactate transporter activity; IEA.
DR GO; GO:0015727; P:lactate transport; IEA.
DR InterPro; IPR003804; Lactate perm.
DR Pfam; PF02652; Lactate_perm; 1.
DR TIGRFAMs; TIGR00795; lctp; 1.
DR Complete proteome.
SQ SEQUENCE 551 AA; 59533 MW; 1168669180CF9A CRC64;

Query Match 60.9%; Score 39; DB 16; Length 551;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLWL 10
Db 8 YDPLGNLWL 16

RESULT 78
ID 09HFY8 PRELIMINARY; PRT; 837 AA.
AC 09HFY8;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Gag protein.
GN Gag.
OS Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella
OS cingulata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes; Incertae sedis; Phyllachorales; Phyllachoraceae;
OC Glomerella.
OX NCBI_TaxID=5457;
RN (1)
RP SEQUENCE FROM N.A.
RC TRANSPOSON=retrotransposon Cgret;
RA Zhu P., Oudemans P.V.;
RT "A long terminal repeat retrotransposon Cgret from the phytopathogenic
RT fungus Colletotrichum gloeosporioides on cranberry."
RL Curr. Genet. 0:0-0(2000)
DR EMBL; AF264028; AAG24791.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR005162; Retrotrans_gag.
DR InterPro; IPR005159; WCCH.
DR InterPro; IPR001878; ZnF_CCHC.
DR Pfam; PF03732; Retrotrans_gag; 1.
DR Pfam; PF03716; WCCH; 3.
DR Pfam; PF00096; ZF_CCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; ZnF_C2HC; 1.
DR PROSITE; PS50158; ZF_CCHC; 1.
SQ SEQUENCE 837 AA; 97738 MW; EF1D4BC70F55003 CRC64;

Query Match 60.9%; Score 39; DB 3; Length 837;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYDPLTKLWL 10
Db 161 WFEPLQDEWL 170

RESULT 79
ID 08A3P6 PRELIMINARY; PRT; 848 AA.
AC 08A3P6;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Conserved hypothetical protein.
```

GN BT2908.
 OS Bacteroides thetaiotaomicron.
 OC Bacteriia; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 ON NCBI_TaxID=818;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=VPI-5482 / ATCC 29148;
 RX MEDLINE=22550858; PubMed=12663928;
 RA Xu J., Bjursell M.K., Himrod U., Deng S., Carmichael L.K.,
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
 RL Science 299:2074-2076(2003).
 DR EMBL; AF016938; AAC78014.1; -
 DR InterPro; IPR006775; DUF608.
 KW Pfam; PF04685; DUF608; 1.
 SQ SEQUENCE 848 AA; 96073 MW; DE776292CE6C68F1 CRC64;

Query Match 60.9%; Score 39; DB 16; Length 848;
 Best Local Similarity 55.6%; Pred. No. 3.8e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WYDLPTKMW 9
 Db 255 WFDLTLWVW 263

RESULT 80
 Q9N172 PRELIMINARY; PRT; 871 AA.
 AC Q9N172;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Pol polyprotein (Fragment).
 GN POL.
 OS Trichosurus vulpecula (Brush-tailed possum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
 ON NCBI_TaxID=9337;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21105294; PubMed=11160757;
 RA Baillie G.J., Wilkins R.J.;
 RT "Endogenous type D retrovirus in a Marsupial, the Common Brushtail
 Possum (Trichosurus vulpecula)."
 RL J. Virol. 75:2499-2507(2001).
 DR EMBL; AF24725; AAF36395.1; -
 DR HSSP; P03355; 1MML.
 DR GO; GO:0004182; F:carboxypeptidase A activity; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0008907; F:integrase activity; IEA.
 DR GO; GO:0004523; F:ribonuclease H activity; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0015074; P:DNA recombination; IEA.
 DR GO; GO:0006310; P:DNA integration; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001037; Integrase_C.
 DR InterPro; IPR000308; Integrase_C.
 DR InterPro; IPR002156; Peptidase_M14.
 DR InterPro; IPR001584; RVE.
 DR InterPro; IPR000477; RVTse.
 DR Pfam; PF00552; Integrase; 1.
 DR Pfam; PF00202; Integrase; 1.
 DR Pfam; PF00075; rnaaseH; 1.
 DR Pfam; PF00665; rve; 1.
 DR Pfam; PF00078; rvc; 1.

DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
 KW Polyprotein; RNA-directed DNA polymerase; Transferase.
 FT NON_TER
 SQ SEQUENCE 871 AA; 98235 MW; 839AE439025C1543 CRC64;

Query Match 60.9%; Score 39; DB 6; Length 871;
 Best Local Similarity 66.7%; Pred. No. 3.9e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDLPTKMW 9
 Db 821 WKDPLTHQW 829

RESULT 81
 Q9TTA5 PRELIMINARY; PRT; 941 AA.
 AC Q9TTA5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE DNA-dependent ATPase A.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE=20179861; PubMed=10713074;
 RA Muthuswami R., Truman P.A., Mesner L.D., Hockensmith J.W.;
 RT "A Eukaryotic SM12/SNP2 Domain, an Exquisite Detector of Double-
 stranded to Single-stranded DNA Transition Elements."
 RL J. Biol. Chem. 275:7648-7655(2000).
 DR EMBL; AF173643; AAF22285.1; -
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR000330; SNP2_N.
 DR Pfam; PF00271; helicase_C_1.
 DR Pfam; PF00176; SNP2_N_2.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC; 1.
 KW ATP-binding; Helicase; Hydrolase.
 SQ SEQUENCE 941 AA; 104915 MW; AC309EF813B931B CRC64;

Query Match 60.9%; Score 39; DB 6; Length 941;
 Best Local Similarity 75.0%; Pred. No. 4.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKMW 9
 Db 267 YDPATKMW 274

RESULT 82
 Q8XX42 PRELIMINARY; PRT; 948 AA.
 AC Q8XX42;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Putative signal peptide protein.
 GN RSC2276 OR RS01282.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 ON NCBI_TaxID=305;
 RN (1)

RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 Ariat M., Billault A., Brottier P., Camus J.C., Caticolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunac S., Demange N.,
 GAudin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weissbach J., Boucher C.A.,
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*,"
 RL Nature 415:497-502 (2002).
 DR EMBL; AL646069; CAD15983.1; -
 KW Complete proteome.
 SQ SEQUENCE 948 AA; 103933 MW; D3ED825F08A8E48 CRC64;

QY Query Match 60.9%; Score 39; DB 16; Length 948;
 Best Local Similarity 60.0%; Pred. No. 4.3e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1 WYDPLTKML 10
 101 WYQALPKAWL 110

RESULT 83
 ID 086585 PRELIMINARY; PRT; 2183 AA.
 AC 086585;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein SCO6220.
 GN SCO6220 OR SC2H4.02.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thompson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,
 RA Hopwood D.A.,
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 coelicolor A3(2).",
 RL Nature 417:141-147 (2002).
 DR EMBL; AL939126; CA20596.1; -
 DR PIR; T37218; T37218.
 DR InterPro; IPR006530; YD.
 DR Pfam; PF05593; RNS_repeat; 6.
 DR TIGRFAMs; TIGR01643; YD_repeat_2x; 9.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 2183 AA; 233388 MW; 373B8EA2BC998FD CRC64;

QY Query Match 60.9%; Score 39; DB 16; Length 2183;
 Best Local Similarity 66.7%; Pred. No. 9.7e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 WYDPLTKML 9
 1942 WYQPLTKOM 1950

RESULT 84
 ID 07UT29 PRELIMINARY; PRT; 277 AA.

AC 07UT29;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN RB4150.
 OS Rhodospirillum rubrum.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Firelulua.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Hellmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.,
 RT "Complete genome sequence of the marine planctomycete *Firelulua* sp.
 strain 1",
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
 DR EMBL; BX294140; CAD73612.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 277 AA; 31373 MW; FABD51A3D984B11C CRC64;

QY Query Match 60.2%; Score 38.5; DB 16; Length 277;
 Best Local Similarity 53.8%; Pred. No. 1.5e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Db 1 WYD--P-LTKML 10
 64 WYDMMBPQKIKML 76

RESULT 85
 ID P71125 PRELIMINARY; PRT; 33 AA.
 AC P71125;
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE lcp protein (Fragment).
 GN LCP.
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=81-176;
 RX MEDLINE=96239019; PubMed=8675309;
 RA Pickett C.L., Pesci E.C., Cottle D.L., Russell G., Erdem A.N.,
 RA Zeytin H.,
 RT "Prevalence of cytolethal distending toxin production in *Campylobacter*
 jejuni and relatedness of *Campylobacter* sp. cdtB gene.",
 RL Infect. Immun. 64:2070-2078 (1996).
 DR EMBL; U51121; AAB06710.1; -
 FT NON_TER
 SQ SEQUENCE 33 AA; 3859 MW; C6A46123212DAF4D CRC64;

QY Query Match 59.4%; Score 38; DB 2; Length 33;
 Best Local Similarity 55.6%; Pred. No. 23;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 2 YDPLTKML 10
 8 YDPSNIML 16

RESULT 86
 ID 08F670 PRELIMINARY; PRT; 43 AA.
 AC 08F670;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)

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DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN LA1169.
OS Leptospiira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AE011300; AAA8368.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 43 AA; 5302 MW; 49473435BFAD790C CRC64;

Query Match
Best Local Similarity 59.4%; Score 38; DB 16; Length 43;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 9
Db 14 FYEPI TKLM 22

RESULT 87
O8W3Q4 PRELIMINARY; PRT; 92 AA.
ID O8W3Q4;
AC O8W3Q4;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Reverse transcriptase (Fragment).
GN NOR3.
OS Silene noctiflora (night-flowering catchfly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=39899;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=Ty1-copia type retrotransposon;
RA Matsunaga S.;
RT "Retrotransposons in the genus Silene."
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB065075; BAB83582.1; -.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 92 AA; 10696 MW; 1040F21BBA53DD89 CRC64;

Query Match
Best Local Similarity 59.4%; Score 38; DB 10; Length 92;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10
Db 51 WYDRLSKLL 60

RESULT 88
O8EUP0 PRELIMINARY; PRT; 140 AA.
ID O8EUP0;
AC O8EUP0;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN MYB8810.
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=28227;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=HF-2;
RX MEDLINE=22354719; PubMed=12466555;
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
RT "The complete genomic sequence of Mycoplasma penetrans, an
RT intracellular bacterial pathogen in humans."
RL Nucleic Acids Res. 30:5293-5300(2002).
DR EMBL: AP004173; BAC44672.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 140 AA; 16102 MW; 67E4A5710F80FAA1 CRC64;

Query Match
Best Local Similarity 59.4%; Score 38; DB 16; Length 140;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 WYDPLTKLML 10
Db 39 YNPITKQWI 47

RESULT 89
O9K9C7 PRELIMINARY; PRT; 190 AA.
ID O9K9C7;
AC O9K9C7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Hypothetical protein BH2722.
GN BH2722.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=2051582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kohara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL: AP001516; BAB06441.1; -.
DR PIR: B83990; B83990.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 190 AA; 21477 MW; 626CE4855E2C3A4F CRC64;

Query Match
Best Local Similarity 59.4%; Score 38; DB 16; Length 190;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10
Db 146 WYDPLTKLML 155

RESULT 90
O27482 PRELIMINARY; PRT; 206 AA.
ID O27482;
AC O27482;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Hypothetical protein MTH1433.
GN MTH1433.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;

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RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J.,
 RA Altriede T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang R., Keagle P., Lunn M., Pochier B., Qiu D.,
 RA Spadator R., Vitcare R., Wang Y., Wierdowski J., Gibson R.,
 RA Jiwani N., Carnes A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McOugall S., Shmer G., Goyal A., Petrovski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of *Methanobacterium thermoautotrophicum*
 RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155 (1997).
 DR EMBL; AE000905; AAB85908.1; -.
 DR PIR; G69057; G69057.
 KW Hypothetical protein: Complete proteome.
 SQ SEQUENCE 206 AA; 21815 MW; 5982982950518AEE CRC64;

Query Match 59.4%; Score 38; DB 17; Length 206;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9
 DB 106 YDPLTSRW 113

RESULT 91
 ID 08A620 PRELIMINARY; PRT; 283 AA.
 AC 08A620;
 DT 01-JUN-2003 (TReMBLrel. 24, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Putative oxidoreductase.
 GN BT2066.
 OS Bacteroides thetaiotaomicron.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=818;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VPI-5482 / ATCC 29148;
 RX MEDLINE=22550858; PubMed=12663928;
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
 RA Chiang H.C., Hooper L.V., Gordon J.I.;
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
 RL Science 289:2074-2076 (2003).
 DR EMBL; AE016934; AAO77173.1; -.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 KW Complete proteome.
 SQ SEQUENCE 283 AA; 31619 MW; BDE4DFB5A3C544 CRC64;

Query Match 59.4%; Score 38; DB 16; Length 283;
 Best Local Similarity 55.6%; Pred. No. 1.9e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
 DB 209 WFDPLTDIF 217

RESULT 92
 ID 016974 PRELIMINARY; PRT; 295 AA.
 AC 016974;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN T02B11.1.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Peloderinae; *Caenorhabditis*.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology. The *C. elegans* Sequencing Consortium.";
 RL Science 282:2012-2018 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Goela D.;
 RT "The sequence of *C. elegans* cosmid T02B11.";
 RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF022979; AAB69903.1; -.
 DR PIR; T32202; T32202.
 DR WormPep; T02B11.1; CE13032.
 KW Hypothetical protein.
 SQ SEQUENCE 295 AA; 34613 MW; 24613CA68A8F8543 CRC64;

Query Match 59.4%; Score 38; DB 5; Length 295;
 Best Local Similarity 85.7%; Pred. No. 2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PLTKLWL 10
 DB 3 PLTKLWL 9

RESULT 93
 ID 09N3X5 PRELIMINARY; PRT; 300 AA.
 AC 09N3X5;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Serpentine receptor, class 9 (Gamma) protein 50.
 GN Y43B11AR.2 OR SRG-50.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; *Caenorhabditis*.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Wilson R.;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology. The *C. elegans* Sequencing Consortium.";
 RL Science 282:2012-2018 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Cordes M., Maupin R.;
 RT "The sequence of *C. elegans* cosmid Y43B11AR.";
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.H.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;


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SQ SEQUENCE 341 AA; 38032 MW; 0AF98BB343B75774 CRC64;
Query Match 59.4%; Score 38; DB 16; Length 341;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DPLTKLW 9
    |||:|
    184 DPLTKLW 190

RESULT 97
08BJT8 PRELIMINARY; PRT; 345 AA.
ID 08BJT8
AC 08BJT8
DT 01-JUN-2003 (TRENBLREL. 24, Created)
DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)
DE GAF domain/GDEF domain protein.
GN PP2505.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Meinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Kouri H., Hance I.,
RA Chris Lee P., Holtzaple E., Scanlan D., Tran K., Moazzez A.,
RA Uterback T., Rizzo M., Lee K., Kosack D., Moesti D., Wedler H.,
RA Lauder J., Stjepandic D., Hohnselt U., Straetz M., Helm S.,
RA Kiewitz C., Eissen J., Timmis K.N., Duesterhoeft A., Tsemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AE016783; AAN68117.1; -.
DR TIGR; PP2505; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008170; F:N-methyltransferase activity; IEA.
DR GO; GO:0006306; P:DNA methylation; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR00160; GDEF.
DR Pfam; PF00590; GAF.1.
DR Pfam; PF00990; GDEF.1.
DR PROSITE; PS00887; GDEF.1.
DR PROSITE; PS00092; N6_MTHSE.1.
DR Complete proteome.
SQ SEQUENCE 345 AA; 38521 MW; 89EC3F871D000D0C CRC64;

Query Match 59.4%; Score 38; DB 16; Length 345;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DPLTKLW 9
    |||:|
    184 DPLTKLW 190

RESULT 98
08JDY9 PRELIMINARY; PRT; 361 AA.
ID 08JDY9
AC 08JDY9
DT 01-MAR-2002 (TRENBLREL. 20, Created)
DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Atrase VIRB11 homolog.
GN BMEI10035.
OS Brucella melitensis.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kaparakis V., Redkar R.J., Patra G., Mijer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykakis A., Reznik G.,
RA Jablonksi L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldstein E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-D.,
RA Haselkorn R., Kyriides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009642; AAL53276.1; -.
DR PIR; A13513; A13513.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR GO; GO:000437; GSP11 E.1.
DR InterPro; IPR001482; GSP11 E.
DR InterPro; IPR002078; S1954_interact.
DR Pfam; PF00437; GSP11 E.1.
DR PROSITE; PS00673; SIGMA54_INTERACT_1; 1.
DR Complete proteome.
SQ SEQUENCE 361 AA; 40723 MW; 43D97E87A99E3B7D CRC64;

Query Match 59.4%; Score 38; DB 16; Length 361;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WYDPLTK 7
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    343 WYDPLTK 349

RESULT 99
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ID 08FXK7
AC 08FXK7
DT 01-MAR-2003 (TRENBLREL. 23, Created)
DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Type IV secretion system protein VirB11.
GN BRA0059.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1330 / Biovar 1;
RX MEDLINE=2247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eissen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Unayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J., Van Aken S.B.,
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AE014510; AAN33271.1; -.
DR TIGR; BRA0059; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR GO; GO:000437; GSP11 E.
DR InterPro; IPR001482; GSP11 E.

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DR InterPro: IPR002078; Sig54_interact.
 DR Pfam: PF00437; GSP1_E; 1.
 DR ProDom: PD000739; GSP1_E; 1.
 DR PROSITE: PS00675; SIGMA54_INTERACT_1; 1.
 KW Complete proteome.
 SQ SEQUENCE 361 AA; 40726 MW; D9DD62F91D2CD3D CRC64;

Query Match 59.4%; Score 38; DB 16; Length 361;
 Best Local Similarity 85.7%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDP1TK 7
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 Db 344 WYDPNTK 350

RESULT 100
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 ID Q9KISS
 AC Q9KISS;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE VIRB1.
 GN VIRB1.
 OS Brucella abortus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxId=235;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2308;
 RX MEDLINE=20398168; PubMed=10940027;
 RA Sieira R., Comercl D.J., Sanchez D.O., Ugalde R.A.;
 RT "A Homologue of an Operon Required for DNA Transfer in Agrobacterium
 RT is Required in Brucella abortus for Virulence and Intracellular
 RT Multiplication.";
 RL J. Bacteriol. 182:4849-4855(2000).
 DR EMBL: AF262678; AAF73904.1; -;
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0005524; P:ATP binding; IEA.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR GO: GO:000160; P:two-component signal transduction system (p. . .; IEA.
 DR InterPro: IPR001482; GSP1_E.
 DR InterPro: IPR002078; Sig54_interact.
 DR Pfam: PF00437; GSP1_E; 1.
 DR ProDom: PD000739; GSP1_E; 1.
 DR PROSITE: PS00675; SIGMA54_INTERACT_1; 1.
 SQ SEQUENCE 362 AA; 40884 MW; 4C32B060F4FC79BD CRC64;

Query Match 59.4%; Score 38; DB 2; Length 362;
 Best Local Similarity 85.7%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDP1TK 7
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 Db 344 WYDPNTK 350

Search completed: July 12, 2004, 21:29:50
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